

FORM PTO-1390 (REV 10-95)		U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE	ATTORNEY'S DOCKET NUMBER
<b>TRANSMITTAL LETTER TO THE UNITED STATES DESIGNATED/ELECTED OFFICE (DO/EO/US) CONCERNING A FILING UNDER 35 U.S.C. §371</b>			SCH 1779 U.S. APPLICATION NO. (If known, use 37 CFR §1.4) <b>097673400</b>
INTERNATIONAL APPLICATION NO.	INTERNATIONAL FILING DATE	PRIORITY DATE CLAIMED	
PCT/DE99/01178	15 April 1999	17 April 1998	
TITLE OF INVENTION			
HUMAN NUCLEIC ACID SEQUENCES FROM HYSTEROMYOMIC TISSUE			
APPLICANT(S) FOR DO/EO/US			
SPECHT, Thomas, et al.			
Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:			
1. <input checked="" type="checkbox"/> This is a <b>FIRST</b> submission of items concerning a filing under 35 U.S.C. §371. 2. <input type="checkbox"/> This is a <b>SECOND</b> or <b>SUBSEQUENT</b> submission of items concerning a filing under 35 U.S.C. §371. 3. <input type="checkbox"/> This express request to begin national examination procedures (35 U.S.C. §371(d)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. §371(b) and PCT Articles 22 and 39(1). 4. <input checked="" type="checkbox"/> A proper Demand for International Preliminary Examination was made by the 19 <sup>th</sup> month from the earliest claimed priority date. 5. <input checked="" type="checkbox"/> A copy of the International Application as filed (35 U.S.C. §371(c)(2)) a. <input type="checkbox"/> is transmitted herewith (required only if not transmitted by the International Bureau). b. <input checked="" type="checkbox"/> has been transmitted by the International Bureau. c. <input type="checkbox"/> is not required, as the application was filed in the United States Receiving Office (RO/US). 6. <input checked="" type="checkbox"/> A translation of the International Application into English (35 U.S.C. §371(c)(2)). <input type="checkbox"/> A copy of the International Search Report (PCT/ISA/210). 7. <input checked="" type="checkbox"/> Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. §371(c)(3)) a. <input type="checkbox"/> are transmitted herewith (required only if not transmitted by the International Bureau). b. <input type="checkbox"/> have been transmitted by the International Bureau. c. <input type="checkbox"/> have not been made; however, the time limit for making such amendments has NOT expired. d. <input checked="" type="checkbox"/> have not been made and will not be made. 9. <input type="checkbox"/> A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. §371(c)(3)). 10. <input type="checkbox"/> An oath or declaration of the inventor(s) (35 U.S.C. §371(c)(4)). 11. <input type="checkbox"/> A copy of the International Preliminary Examination Report (PCT/IPEA/409). 12. <input type="checkbox"/> A translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. §371(c)(5)). <b>Items 13. to 19. below concern document(s) or information included:</b> 13. <input type="checkbox"/> An Information Disclosure Statement under 37 C.F.R. §§1.97 and 1.98. 14. <input type="checkbox"/> An assignment document for recording. A separate cover sheet in compliance with 37 C.F.R. §§3.28 and 3.31 is included. 15. <input checked="" type="checkbox"/> A FIRST preliminary amendment. <input type="checkbox"/> A SECOND or SUBSEQUENT preliminary amendment. 16. <input type="checkbox"/> A substitute specification. 17. <input type="checkbox"/> A change of power of attorney and/or address letter. 18. <input type="checkbox"/> Certificate of Mailing by Express Mail 19. <input type="checkbox"/> Other items or information:			

U.S. APPLICATION NO. 09/673400		INTERNATIONAL APPLICATION NO. PCT/DE99/01178		ATTORNEY'S DOCKET NUMBER SCH 1779	
17. <input checked="" type="checkbox"/> The following fees are submitted: <b>BASIC NATIONAL FEE (37 CFR §1.492 (a) (1) - (5)):</b> Search Report has been prepared by the EPO or JPO..... \$860.00 International preliminary examination fee paid to USPTO (37 CFR §1.482)..... \$690.00 No international preliminary examination fee paid to USPTO (37 CFR §1.482) but international search fee paid to USPTO (37 CFR §1.445(a)(2))..... \$710.00 Neither international preliminary examination fee (37 CFR §1.482) nor international search fee (37 CFR §1.445(a)(2)) paid to USPTO..... \$1,000.00 International preliminary examination fee paid to USPTO (37 CFR §1.482) and all claims satisfied provisions of PCT Article 33(2)-(4)..... \$100.00 <b>ENTER APPROPRIATE BASIC FEE AMOUNT =</b> \$860.00				<b>CALCULATIONS</b> PTO USE ONLY	
Surcharge of <b>\$130.00</b> for furnishing the oath or declaration later than months from the earliest claimed priority date (37 C.F.R. §1.492(e)). <input type="checkbox"/> 20 <input type="checkbox"/> 30				\$0.00	
CLAIMS	NUMBER FILED	NUMBER EXTRA	RATE		
Total claims	38 - 20 =	18	x \$ 18.00	\$324.00	
Independent claims	6 - 3 =	3	x \$ 80.00	\$240.00	
MULTIPLE DEPENDENT CLAIM(S) (if applicable)			+ \$ 270.00		
<b>TOTAL OF ABOVE CALCULATIONS =</b>				\$1,424.00	
Reduction of ½ for filing by small entity, if applicable. A Verified Small Entity Statement must also be filed (Note 37 C.F.R. §§1.9, 1.27, 1.28).					
<b>SUBTOTAL =</b>				\$1,424.00	
Processing fee of <b>\$130.00</b> for furnishing the English translation later than months from the earliest claimed priority date (37 C.F.R. §1.492(f)). <input type="checkbox"/> 20 <input type="checkbox"/> 30					
<b>TOTAL NATIONAL FEE =</b>				\$1,424.00	
Fee for recording the enclosed assignment (37 C.F.R. §1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 C.F.R. §§3.28, 3.31). \$40.00 per property.					
<b>TOTAL FEES ENCLOSED =</b>				\$1,424.00	
				Amount to be refunded:	
				charged:	
a. <input checked="" type="checkbox"/> A check in the amount of <u>\$1,424.00</u> to cover the above fees is enclosed. b. <input type="checkbox"/> Please charge my Deposit Account No. <u>13-3402</u> in the amount of \$_____ to cover the above fees. A duplicate copy of this sheet is enclosed. c. <input checked="" type="checkbox"/> The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. <u>13-3402</u> . A duplicate copy of this sheet is enclosed.					
<b>NOTE: Where an appropriate time limit under 37 C.F.R. §§1.494 or 1.495 has not been met, a petition to revive (37 C.F.R. §1.137(a) or (b)) must be filed and granted to restore the application to pending status.</b>					
SEND ALL CORRESPONDENCE TO:					
MILLEN, WHITE, ZELANO & BRANIGAN, P.C.					
Arlington Courthouse Plaza I					
2200 Clarendon Boulevard, Suite 1400					
Arlington, Virginia 22201					
(703) 243-6333					
Filed: October 17, 2000					
aek:k\pat\sch\1779\intl phase transmlt					
				SIGNATURE	
				Anthony J. Zelano	
				NAME	
				27,969	
				REGISTRATION NUMBER	

**IN THE UNITED STATES DESIGNATED/ELECTED OFFICE**

International Application No. : PCT/DE99/01178  
International Filing Date : 15 April 1999  
Priority Date(s) Claimed : 17 April 1998  
Applicant(s) (DO/EO/US) : SPECHT, Thomas, et al.  
Title: HUMAN NUCLEIC ACID SEQUENCES FROM HYSTEROMYOMIC TISSUE

**PRELIMINARY AMENDMENT**

Commissioner for Patents  
Washington, D.C. 20231

Sir:

Prior to calculating the national fee, and prior to examination in the National Phase of the above-identified International application, please amend this application as follows:

**IN THE CLAIMS:**

Claims 5 and 6, line 1: Change "claims 1 to 4" to -- claim 3 --.

Claim 7: Please rewrite as follows:

7. (Amended) A nucleic acid sequence comprising a portion of the nucleic acid sequences named in claim[s 1 to 6]3, in such a sufficient amount that they hybridize with the sequences [according to claims 1 to 6] of claim 3 or a sequence having 90% homology thereto.

Claims 8 and 9, line 1: Change "claims 1 to 7" to -- claim 3 --.

Claim 10, lines 1 and 2: Change "claims 1 to 9" to -- claim 3 --.

Claim 11, line 2: Change "claims 1 to 9" to -- claim 3 --.

Claim 13, lines 1 and 2: Change "claims 11 and 12" to -- claim 11 --.

Claim 14, lines 1 and 2: Change "claims 1 to 10" to -- claim 3 --.

Claim 16, line 3: Change "claims 1 to 10" to -- claim 3 --.

Claim 18, line 1: Change "claims 16 or 17" to -- claim 16 --.

Claim 19, line 2: Change "claims 16 to 18" to -- claim 16 --.

Claim 27, line 2: After "53-55" insert -- of claim 23 --.

Claim 28, line 2: After "52" insert -- of claim 3 --.  
Claim 29, line 2: After "52" insert -- of claim 3 --.  
Claims 30 and 31, line 2: After "53-55" insert -- of claim 23 --.  
Claim 32, line 3: After "53-55" insert -- of claim 23 --.  
Claims 33 and 34, line 1: Change "claims 1 to 10" to -- claim 3 --.  
Claim 35 line 4: After "52" insert -- of claim 3 --.  
Claim 38, line 1: Change "claims 1 to 7" to -- claim 3 --.

### Remarks

The purpose of this Preliminary Amendment is to eliminate multiple and improper multiple dependent claims to avoid additional fees. Applicants reserve the right to reintroduce claims directed to canceled combined subject matter.

Respectfully submitted,

  
\_\_\_\_\_  
Anthony J. Zelano, Reg. No. 27,969  
Attorney for Applicants  
MILLEN, WHITE, ZELANO & BRANIGAN, P.C.  
Arlington Courthouse Plaza 1  
2200 Clarendon Boulevard, Suite 1400  
Arlington, VA 22201  
Direct Dial: 703-812-5311  
Facsimile: 703-243-6410  
Email: zelano@mwzb.com

AJZ:aek  
Filed: OCTOBER 17, 2000  
k:\pat\sch\1779\prelim amdt

Published

Without international search report and to be republished  
after receipt of the report.

(54) **Title: HUMAN NUCLEIC ACID SEQUENCES FROM HYSTEROMYOMIC  
TISSUE**

(57) **Abstract**

Human nucleic acid sequences -- mRNA, cDNA, genomic  
sequences -- from hysteryomyomic tissue, which code for gene  
products or portions thereof, and their use, are described. In  
addition, the polypeptides that can be obtained by way of the  
sequences and their use are described.

### Human Nucleic Acid Sequences from Hysteromyomic Tissue

The invention relates to human nucleic acid sequences from hysteromyomic tissue, which code for gene products or portions thereof, their functional genes that code at least one bioactive polypeptide and their use.

In addition, the invention relates to the polypeptides that can be obtained by way of the sequences and their use.

One of the main causes of death by cancer in women is hysteromyoma, for control of which new therapies are necessary. Previously used therapies, such as, e.g., chemotherapy, hormone therapy or surgical removal of tumor tissue, frequently do not result in a complete cure.

The cancer phenomenon often goes along with overexpression or underexpression of certain genes in degenerated cells, it still being unclear whether these altered expression rates are the cause or the result of the malignant transformation. Identification of these genes would be an important step for development of new therapies against cancer. Spontaneous formation of cancer is often preceded by a host of mutations. They can have the most varied effects on the expression pattern in the affected tissue, such as, e.g., underexpression or overexpression, but also expression of shortened genes. Several such changes due to these mutation cascades can ultimately lead to malignant degeneration. The complexity of these relationships makes an experimental approach very difficult.

0573400-12700

00673400.122700

A database that consists of so-called ESTs is used to look for candidate genes, i.e., genes that compared to the tumor tissue are more strongly expressed in normal tissue. ESTs (expressed sequence tags) are sequences of cDNAs, i.e., mRNAs transcribed in reverse, therefore molecules that reflect gene expression. The EST sequences are determined for normal and degenerated tissue. These databases are offered to some extent commercially by various companies. The ESTs of the LifeSeq database, which is used here, are generally between 150 and 350 nucleotides long. They represent a pattern that is unmistakable for a certain gene, although this gene is normally very much longer (> 2000 nucleotides). By comparison of the expression patterns of normal and tumor tissue, ESTs can be identified that are important for tumor formation and proliferation. There is, however, the following problem: Since the EST sequences that are found can belong to different regions of an unknown gene due to different constructions of cDNA libraries, in this case a completely incorrect ratio of the occurrence of these ESTs in the respective tissue would arise. This would only be noticed when the complete gene is known and thus ESTs can be assigned to the same gene.

It has now been found that this possibility of error can be reduced if all ESTs from the respective tissue type are assembled beforehand, before the expression patterns are compared to one another. Overlapping ESTs of the same gene were thus combined into longer sequences (see Figure 1, Figure 2a and Figure 3). This lengthening and thus coverage of an essentially larger gene

region in each of the respective bases are intended to largely avoid the above-described error. Since there were no existing software products for this purpose, programs for assembling genomic sections were employed, which were used modified and to which our own programs were added. A flow chart of the assembly procedure is shown in Figures 2b1-2b4.

Nucleic acid sequences Seq. ID No. 1 to Seq. ID No. 31 and Seq. ID 52, which play a role as candidate genes in the hysteryoma, have now been found.

Nucleic acid sequences Seq. ID Nos. 14-18, 30, 31 and 52 are of special interest.

The invention thus relates to nucleic acid sequences that code a gene product or a portion thereof, comprising

- a) a nucleic acid sequence selected from the group of nucleic acid sequences Seq. ID Nos. 14-18, 30, 31 and 52.
- b) an allelic variation of the nucleic acid sequences named under a)

or

- c) a nucleic acid sequence that is complementary to the nucleic acid sequences named under a) or b).

In addition, the invention relates to a nucleic acid sequence according to one of the sequences Seq. ID Nos. 14-18, 30, 31 or a complementary or allelic variant thereof and the nucleic acid sequences thereof, which have 90% to 95% homology to a human nucleic acid sequence.

00573400-122700



The invention also relates to nucleic acid sequences Seq. ID No. 1 to Seq. ID No. 31 and Seq. ID 52, which are expressed elevated in the hysteryomyoma.

The invention further relates to nucleic acid sequences comprising a portion of the above-mentioned nucleic acid sequences in such a sufficient amount that they hybridize with sequences Seq. ID Nos. 14-18, 30, 31 and 52.

The nucleic acid sequences according to the invention generally have a length of at least 50 to 4500 bp, preferably a length of at least 150 to 4000 bp, especially a length of 450 to 3500 bp.

With the partial sequences Seq. ID Nos. 14-18, 30, 31 and 52 according to the invention, expression cassettes can also be built using current process practice, whereby on the cassette at least one of the nucleic acid sequences according to the invention is combined with at least one control or regulatory sequence generally known to one skilled in the art, such as, e.g., a suitable promoter. The sequences according to the invention can be inserted in a sense or antisense orientation.

A large number of expression cassettes or vectors and promoters which can be used are known in the literature.

Expression cassettes or vectors are defined as:

1. bacterial, such as, e.g., phagescript, pBs,  $\phi$ X174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene), pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia),
2. eukaryotic, such as, e.g., pWLneo, pSV2cat, pOG44, pXT1, pSG (Stratagene), pSVK3, pBPV, pMSG, pSVL (Pharmacia).

007221 007220

Control or regulatory sequences are defined as suitable promoters. Here, two preferred vectors are the pKK232-8 and the PCM7 vector. In particular, the following promoters are intended: lacI, lacZ, T3, T7, gpt, lambda P<sub>R</sub>, trc, CMV, HSV thymidine-kinase, SV40, LTRs from retrovirus and mouse metallothionein-I.

The DNA sequences located on the expression cassette can code a fusion protein which comprises a known protein and a bioactive polypeptide fragment.

The expression cassettes are likewise the subject matter of this invention.

The nucleic acid fragments according to the invention can be used to produce full-length genes. The genes that can be obtained are likewise the subject matter of this invention.

The invention also relates to the use of the nucleic acid sequences according to the invention and the gene fragments that can be obtained from use.

The nucleic acid sequences according to the invention can be moved with suitable vectors into host cells, in which as the heterologous part, the genetic information which is contained on the nucleic acid fragments and which is expressed is located.

The host cells containing the nucleic acid fragments are likewise the subject matter of this invention.

Suitable host cells are, e.g., prokaryotic cell systems such as E. coli or eukaryotic cell systems such as animal or human cells or yeasts.

00573400-122700  
007221-006260

Production of polypeptides or their fragments is done by cultivation of the host cells according to current cultivation methods and subsequent isolation and purification of the peptides or fragments, likewise using current methods. The invention further relates to nucleic acid sequences, which code at least a partial sequence of a bioactive polypeptide.

The invention further relates to the polypeptide sequences that have at least 80% homology, especially 90% homology to the polypeptide partial sequences of ORF ID Nos. 32-51 and ORF ID Nos. 53-55 according to the invention.

The invention also relates to antibodies that are directed against a polypeptide or a fragment thereof and that are coded by the nucleic acids of sequences Seq. ID Nos. 1-31 and Seq. ID No. 52 according to the invention.

Antibodies are defined especially as monoclonal antibodies.

The antibodies according to the invention can be identified by, i.a., a phage display process. These antibodies are also the subject matter of the invention.

The polypeptide partial sequences according to the invention can be used in a phage display process. The polypeptides that are identified with this process and that bind to the polypeptide

partial sequences according to the invention are also the subject matter of the invention.

The nucleic acid sequences according to the invention can also be used in a phage display process.

The polypeptides of sequences Seq. ID Nos. 32-51 and Seq. ID Nos. 53-55 according to the invention can also be used as tools for finding active ingredients against hystero myoma, which is likewise the subject matter of this invention.

Likewise the subject matter of this invention is the use of nucleic acid sequences according to sequences Seq. ID No. 1 to Seq. ID No. 31 and Seq. ID 52 for expression of polypeptides, which can be used as tools for finding active ingredients against hystero myoma.

The invention also relates to the use of the found polypeptide partial sequences Seq. ID No. 32 to Seq. ID No. 51 and Seq. ID Nos. 53-55 as pharmaceutical agents in the gene therapy for treatment of hystero myoma or for the production of a pharmaceutical agent for treatment of hystero myoma.

The invention also relates to pharmaceutical agents that contain at least one polypeptide partial sequence Seq. ID Nos. 32 to 51 and Seq. ID Nos. 53-55.

The nucleic acid sequences found according to the invention can also be genomic or mRNA sequences.

The invention also relates to genomic genes, their exon and intron structures and their splice variants that can be obtained from cDNAs of sequences Seq. ID Nos. 1-31, and 52, and their use

00673400.122700

together with suitable regulatory elements, such as suitable promoters and/or enhancers.

With the nucleic acids according to the invention (cDNA sequences) Seq. ID Nos. 1-31 and 52, genomic BAC, PAC and cosmid libraries are screened, and specifically human clones are isolated via complementary base pairing (hybridization). The BAC, PAC and cosmid clones isolated in this way are hybridized using fluorescence-in-situ hybridization on metaphase chromosomes, and the corresponding chromosome sections on which the corresponding genomic genes lie are identified. BAC, PAC and cosmid clones are sequenced in order to clarify the corresponding genomic genes in their complete structure (promoters, enhancers, silencers, exons and introns). BAC, PAC and cosmid clones can be used as independent molecules for gene transfer (see Figure 5).

The invention also relates to BAC, PAC and cosmid clones containing functional genes and their chromosomal localization according to sequences Seq. ID Nos. 1-31 and 52, for use as vehicles for gene transfer.

09573400.122700

## Meanings of Technical Terms and Abbreviations

Nucleic acids= Nucleic acids in this invention are defined as:

mRNA, partial cDNA, full-length cDNA and genomic genes (chromosomes)

ORF = Open Reading Frame, a defined sequence of amino acids which can be derived from the cDNA sequence

Contig = A set of DNA sequences that can be combined as a result of very great similarities into one sequence (consensus)

Singleton = A contig that contains only one sequence

Module = Domain of a protein with a defined sequence, which represents one structural unit and which occurs in various proteins

N = selectively the nucleotide A, T, G or C

X = selectively one of the 20 naturally occurring amino acids

## Explanation of the Alignment Parameters

minimal initial match = minimal initial identity area

maximum pads per read = maximum number of insertions

maximum percent mismatch = maximum deviation in %

## Explanation of Figures

Figure 1 shows the systematic gene search in the Incyte LifeSeq database

Figure 2a shows the principle of EST assembling

Figures 2b1-2b4 show the entire principle of EST assembling

00673400.1.000000

- Figure 3 shows the in-silico subtraction of gene expression in various tissues
- Figure 4a shows the determination of tissue-specific expression via electronic Northern
- Figure 4b shows the electronic Northern
- Figure 5 shows the isolation of genomic BAC and PAC clones.

00673400.122700

The following examples explain the production of the nucleic acid sequences according to the invention without limiting the invention to these examples and nucleic acid sequences.

### **Example 1**

#### **Search for Tumor-related Candidate Genes**

First, all ESTs of the corresponding tissue from the LifeSeq database (from October 1997) were extracted. They were then assembled by means of the GAP4 program of the Staden package with the parameters 0% mismatch, 8 pads per read and a minimal match of 20. The sequences (fails) not recorded in the GAP4 database were assembled first at 1% mismatch and then again at 2% mismatch with the database. Consensus sequences were computed from the contigs of the database that consisted of more than one sequence. The singletons of the database, which consisted of only one sequence, were re-assembled at 2% mismatch with the sequences not recorded in the GAP4 database. In turn, the consensus sequences were determined for the contigs. All other ESTs were re-assembled at 4% mismatch. The consensus sequences were extracted once again and finally assembled with the previous consensus sequences and the singletons and the sequences not recorded in the database at 4% mismatch. The consensus sequences were formed and used with the singletons and fails as the initial basis for tissue comparisons. This procedure ensured that among the parameters used, all sequences represented gene regions independent of one another.

06573400.1.22700



Figures 2b1-2b4 illustrate the lengthening of the hysteronymic tissue ESTs.

The sequences of the respective tissue assembled in this way were then compared to one another by means of the same program (Figure 3). To do this, first all sequences of the first tissue were input into the database. (It was therefore important that they were independent of one another.)

Then, all sequences of the second tissue were compared to all those of the first. The result was sequences that were specific to the first or the second tissue as well as those which occurred in both. In the latter, the ratio of the frequency of occurrence in the respective tissue was evaluated. All programs pertaining to the evaluation of the assembled sequences were themselves developed.

All sequences that occurred more than four times in respectively one of the compared tissues and all that occurred at least five times as often in one of the two tissues were further studied. These sequences were subjected to an electronic Northern (see Example 2.1), by which the distribution in all tumor and normal tissues was studied (see Figure 4a and Figure 4b). The relevant candidates were then lengthened using all Incyte ESTs and all ESTs of public databases (see Example 3). Then, the sequences and their translation into possible proteins were compared to all nucleotide and protein databases and were studied for possible regions that code for proteins.

**Example 2****Algorithm for Identification and Lengthening of Partial cDNA Sequences with Altered Expression Pattern**

An algorithm for finding overexpressed or underexpressed genes will be explained below. The individual steps are also summarized in a flow chart for the sake of clarity (see Figure 4b).

**2.1. Electronic Northern Blot**

By means of a standard program for homology search, e.g., BLAST (Altschul, S. F.; Gish, W.; Miller, W.; Myers, E. W. and Lipman, D. J. (1990) J. Mol. Biol. 215, 403-410), BLAST2 (Altschul, S. F.; Madden, T. L.; Schäffer, A. A.; Zhang, J.; Zhang, Z.; Miller, W., and Lipman, D. J. (1997) Nucleic Acids Research 25 3389-3402) or FASTA (Pearson, W. R. and Lipman, D. J. (1988) Proc. Natl. Acad. Sci. USA 85 2444-2448), the homologous sequences in various EST libraries (private or public) arranged by tissues are determined for a partial DNA sequence S, e.g., an individual EST or a contig of ESTs. The (relative or absolute) tissue-specific occurrence frequencies of this partial sequence S which were determined in this way are called electronic Northern Blots.

00221-0042-000

**2.1.1**

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 30 was found, which occurs more frequently in the hysteryomic tissue than in normal tissue.

The result is as follows:

09673400.122700

096740-12700

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
	Breast	
0.0000	Ovary_n	0.0000
0.0000	Ovary_t	0.0000
0.0000	Endocrine tissue	0.0000
0.0000	Fetal	0.0000
0.0000	Gastrointestinal	0.0000
0.0000	Hematopoietic	0.0000
0.0000	Skin-muscle	0.0000
0.0000	Testicles	0.0000
0.0000	Lung	0.0000
0.0000	Nerves	0.0000
0.0000	Prostate	0.0000
0.0000	Sensory Organs	0.0000
0.0000	Uterus_n	0.0000

**2.1.2.**

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 31 was found, which occurs more frequently in the hysteryomic tissue than in normal tissue.

The result is as follows:

09673400.122700

Electronic Northern for SEQ. ID NO.: 31

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0051	0.0000	undef
Breast	0.0038	0.0019	2.0416	0.4898
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0030	0.0104	0.2878	3.4745
Endocrine tissue	0.0034	0.0100	0.3396	2.9444
Gastrointestinal	0.0057	0.0046	1.2425	0.8048
Brain	0.0111	0.0051	2.1599	0.4630
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0095	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0042	0.0102	0.4064	2.4505
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0050	0.5711	1.7510
Kidney	0.0163	0.0058	2.3791	0.4203
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0090	0.0000	undef	0.0000
Prostate	0.0022	0.0021	1.0236	0.9769
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0340	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0224			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0061			
Cervix	0.0213			

FETUS	STANDARDIZED/SUBTRACTED	
% frequency	LIBRARIES	
	% frequency	
	Breast	0.0000
0.0000	Ovary_n	0.0000
0.0028	Ovary_t	0.0000
0.0125	Endocrine tissue	0.0000
0.0000	Fetal	0.0000
0.0000	Gastrointestinal	0.0000
0.0000	Hematopoietic	0.0000
0.0036	Skin-muscle	0.0000
0.0036	Testicles	0.0000
0.0254	Lung	0.0000
0.0062	Nerves	0.0000
0.0303	Prostate	0.0000
0.0000	Sensory Organs	0.0000
0.0125	Uterus_n	0.0000

09573400.122700

In an analogous procedure, the following Northern were also found:

Electronic Northern for SEQ. ID NO.: 1

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0468	0.0562	0.8321	1.2018
Breast	0.0576	0.0752	0.7556	1.3062
Small intestine	0.0766	0.0662	1.1586	0.8631
Ovary	0.0509	0.0650	0.7829	1.2774
Endocrine tissue	0.0596	0.0702	0.8491	1.1778
Gastrointestinal	0.0690	0.1203	0.5735	1.7438
Brain	0.0850	0.0873	0.9741	1.0266
Hematopoietic	0.0722	0.0379	1.9056	0.5248
Skin	0.0918	0.0000	undef	0.0000
Hepatic	0.0143	0.1100	0.1298	7.7066
Heart	0.1123	0.0275	4.0862	0.2447
Testicles	0.0518	0.0819	0.6325	1.5809
Lung	0.1080	0.0879	1.2287	0.8138
Stomach-esophagus	0.0676	0.0307	2.2059	0.4533
Muscle-skeleton	0.0737	0.0790	0.9445	1.0587
Kidney	0.0407	0.0890	0.4575	2.1857
Pancreas	0.0463	0.0552	0.8376	1.1939
Penis	0.0449	0.0000	undef	0.0000
Prostate	0.0436	0.0554	0.7874	1.2700
Uterus-endometrium	0.0338	0.0554	0.6000	0.0000
Uterus-myometrium	0.0534	0.1426	0.3741	2.6732
Uterus-general	0.0255	0.0000	undef	0.0000
Breast hyperplasia	0.0863			
Prostate hyperplasia	0.0535			
Seminal vesicle	0.0890			
Sensory organs	0.0588			
White blood cells	0.0772			
Cervix	0.1171			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0139	Breast	0.0204
Gastrointestinal	0.0583	Ovary_n	0.1595
Brain	0.0500	Ovary_t	0.0051
Hematopoietic	0.0590	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0256
Hepatic	0.0000	Gastrointestinal	0.0488
Heart-blood vessels	0.0462	Hematopoietic	0.0000
Lung	0.0578	Skin-muscle	0.0227
Suprarenal gland	0.0254	Testicles	0.0154
Kidney	0.0679	Lung	0.0082
Placenta	0.0545	Nerves	0.0191
Prostate	0.2493	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

00673400.122700

## Electronic Northern for SEQ. ID NO.: 2

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0039	0.0102	0.3814	2.6222
Small intestine	0.0128	0.0038	3.4026	0.2939
Ovary	0.0031	0.0165	0.1854	5.3946
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0017	0.0075	0.2264	4.4166
Brain	0.0019	0.0093	0.2071	4.8289
Hematopoietic	0.0022	0.0103	0.2160	4.6299
Skin	0.0040	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0065	0.0000	undef
Testicles	0.0058	0.0137	0.0771	12.9706
Lung	0.0021	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0082	0.2540	3.9367
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0054	0.0120	0.0000	undef
Pancreas	0.0000	0.0000	undef	0.0000
Penis	0.0030	0.0055	0.0000	undef
Prostate	0.0000	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0021	0.0000	undef
Uterus-myometrium	0.0000	0.0528	0.0000	undef
Uterus-general	0.0051	0.0408	0.0000	undef
Breast hyperplasia	0.0064	0.0534	0.0534	18.7357
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0009			
Cervix	0.0000			

FETUS  
% frequency

Development	
Gastrointestinal	0.0974
Brain	0.0333
Hematopoietic	0.0063
Skin	0.0157
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0249
Suprarenal gland	0.0325
Kidney	0.0761
Placenta	0.0618
Prostate	0.0727
Sensory organs	0.0249
	0.0000

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0384
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0259
Testicles	0.0000
Lung	0.0328
Nerves	0.0171
Prostate	0.0137
Sensory Organs	0.0000
Uterus_n	0.0083

09673400.122700



Electronic Northern for SEQ. ID NO.: 3

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.1163	undef	undef
Gastrointestinal	0.0000	0.0000	0.0000	undef
Brain	0.0140	0.0010	undef	undef
Hematopoietic	0.0000	0.0000	13.6792	0.0731
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0815	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0028	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0090
Prostate	0.0000	Prostate	0.0137
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

00673400.122700

Electronic Northern for SEQ. ID NO.: 4

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N

Bladder	0.0078	0.0077	1.0170	0.9833
Breast	0.0026	0.0038	0.6805	1.4694
Small intestine	0.0031	0.0163	0.1854	5.3946
Ovary	0.0060	0.0026	2.3025	0.4343
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0046	0.0000	undef
Brain	0.0007	0.0031	0.2400	4.1669
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.1695	0.0000	undef
Hepatic	0.0095	0.0412	0.2313	4.3215
Heart	0.0000	0.0000	undef	undef
Testicles	0.0021	0.0041	0.5080	1.9684
Lung	0.0000	0.0077	0.0000	undef
Stomach-esophagus	0.0017	0.0120	0.1428	7.0040
Muscle-skeleton	0.0027	0.0000	undef	0.0000
Kidney	0.0033	0.0055	0.5983	1.6714
Pancreas	0.0030	0.0000	undef	0.0000
Penis	0.0000	0.0021	0.0000	undef
Prostate	0.0068	0.0000	undef	0.0000
Uterus-endometrium	0.0152	0.0893	0.1727	5.7919
Uterus-myometrium	0.0051	0.0000	undef	0.0000
Uterus-general	0.0032			
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0118			
Sensory organs	0.0000			
White blood cells	0.0000			
cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0068
Gastrointestinal	0.0278	Ovary_n	0.0000
Brain	0.0139	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0093
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0213	Skin-muscle	0.0130
Suprarenal gland	0.0253	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0185	Nerves	0.0000
Prostate	0.0061	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
	0.0000	Uterus_n	0.0000

00673400.122700

## Electronic Northern for SEQ. ID NO.: 5

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0390	0.0332	1.1734	0.8522
Small intestine	0.0345	0.0414	0.8352	1.1973
Ovary	0.0399	0.0662	0.6024	1.6599
Endocrine tissue	0.0359	0.0546	0.6579	1.5201
Gastrointestinal	0.0528	0.0351	1.5040	0.6649
Brain	0.0172	0.0185	0.9319	1.0731
Hematopoietic	0.0214	0.0359	0.5965	1.6763
Skin	0.0294	0.0379	0.7763	1.2881
Hepatic	0.0257	0.1695	0.1516	6.5954
Heart	0.0476	0.0323	1.4706	0.6800
Testicles	0.0276	0.0000	undef	0.0000
Lung	0.0633	0.0234	2.7059	0.3696
Stomach-esophagus	0.0312	0.0266	1.1724	0.8530
Muscle-skeleton	0.0387	0.0153	2.5211	0.3967
Kidney	0.0308	0.0360	0.8567	1.1673
Pancreas	0.0326	0.0548	0.5948	1.6813
Penis	0.0132	0.0221	0.5983	1.6714
Prostate	0.0479	0.0000	undef	0.0000
Uterus-endometrium	0.0153	0.0319	0.4777	2.0934
Uterus-myometrium	0.0473	0.0528	0.8962	1.1158
Uterus-general	0.0305	0.1019	0.2993	3.3415
Breast hyperplasia	0.0560	0.1908	0.2936	3.4065
Prostate hyperplasia	0.0448			
Seminal vesicle	0.0446			
Sensory organs	0.1513			
White blood cells	0.0235			
Cervix	0.0061			
	0.0426			

FETUS  
% frequency

Development	
Gastrointestinal	0.0974
Brain	0.0222
Hematopoietic	0.0000
Skin	0.0197
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0356
Suprarenal gland	0.0325
Kidney	0.0000
Placenta	0.0185
Prostate	0.0909
Sensory organs	0.1496
	0.0126

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	0.0136
Ovary_n	0.0000
Ovary_t	0.0051
Endocrine tissue	0.0000
Fetal	0.0099
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0324
Testicles	0.0231
Lung	0.0328
Nerves	0.0131
Prostate	0.0068
Sensory Organs	0.0077
Uterus_n	0.0208

0967340.122700

Electronic Northern for SEQ. ID NO.: 6

	NORMAL	TUMOR	Ratios	T/N
	% frequency	% frequency	N/T	
Bladder	0.0429	0.1278	0.3356	2.9798
Breast	0.1036	0.1203	0.8613	1.1610
Small intestine	0.0215	0.0992	0.2163	4.6240
Ovary	0.0599	0.0702	0.8528	1.1726
Endocrine tissue	0.0783	0.0426	1.8380	0.5441
Gastrointestinal	0.0249	0.0786	0.3167	3.1574
Brain	0.0429	0.1284	0.3341	2.9935
Hematopoietic	0.0227	0.1136	0.2000	5.0008
Skin	0.0844	0.1695	0.4982	2.0073
Hepatic	0.0523	0.0712	0.7353	1.3600
Heart	0.0922	0.1649	0.5590	1.7890
Testicles	0.0460	0.0585	0.7872	1.2704
Lung	0.0447	0.0797	0.5601	1.7853
Stomach-esophagus	0.0000	0.0537	0.0000	undef
Muscle-skeleton	0.1490	0.1380	1.0801	0.9258
Kidney	0.0489	0.0479	1.0196	0.9808
Pancreas	0.0149	0.1049	0.1417	7.0571
Penis	0.0509	0.1333	0.3819	2.6187
Prostate	0.0196	0.0319	0.6142	1.6282
Uterus-endometrium	0.0676	0.1583	0.4268	2.3432
Uterus-myometrium	0.0381	0.3260	0.1169	8.5541
Uterus-general	0.0560	0.0000	undef	0.0000
Breast hyperplasia	0.0863			
Prostate hyperplasia	0.0297			
Seminal vesicle	0.0089			
Sensory organs	0.0353			
White blood cells	0.0078			
Cervix	0.0213			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	
Gastrointestinal	0.1670	Ovary_n	0.0476
Brain	0.1444	Ovary_t	0.1595
Hematopoietic	0.0125	Endocrine tissue	0.0203
Skin	0.0629	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0379
Heart-blood vessels	0.0000	Hematopoietic	0.0122
Lung	0.0899	Skin-muscle	0.0000
Suprarenal gland	0.0759	Testicles	0.0486
Kidney	0.2535	Lung	0.0077
Placenta	0.1112	Nerves	0.0164
Prostate	0.1091	Prostate	0.0251
Sensory organs	0.1247	Sensory Organs	0.0068
	0.1004	Uterus_n	0.0155
			0.0167

00673400.122700

## Electronic Northern for SEQ. ID NO.: 7

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0117	0.0051	2.2882	0.4370
Breast	0.0128	0.0075	1.7013	0.5879
Small intestine	0.0153	0.0331	0.4634	2.1579
Ovary	0.0150	0.0104	1.4391	0.6949
Endocrine tissue	0.0083	0.0050	1.6981	0.5889
Gastrointestinal	0.0096	0.0278	0.3451	2.8974
Brain	0.0059	0.0113	0.5236	1.9098
Hematopoietic	0.0254	0.0000	undef	0.0000
Skin	0.0257	0.0000	undef	0.0000
Hepatic	0.0143	0.0194	0.7353	1.3600
Heart	0.0106	0.0000	undef	0.0000
Testicles	0.0058	0.0234	0.2460	4.0652
Lung	0.0104	0.0245	0.4234	2.3620
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0051	0.0360	0.1428	7.0040
Kidney	0.0244	0.0068	3.5687	0.2802
Pancreas	0.0083	0.0000	undef	0.0000
Penis	0.0180	0.0000	undef	0.0000
Prostate	0.0219	0.0064	3.4121	0.2931
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0408	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0192			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0089			
Sensory organs	0.0235			
White blood cells	0.0208			
Cervix	0.0213			

FETUS  
% frequency

Development	
Gastrointestinal	0.0278
Brain	0.0083
Hematopoietic	0.0125
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0071
Suprarenal gland	0.0016
Kidney	0.0000
Placenta	0.0309
Prostate	0.0061
Sensory organs	0.0249
	0.0000

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0101
Fetal	0.0245
Gastrointestinal	0.0093
Hematopoietic	0.0122
Skin-muscle	0.0342
Testicles	0.0097
Lung	0.0154
Nerves	0.0082
Prostate	0.0080
Sensory Organs	0.0000
Uterus_n	0.0042

00221 0042260

Electronic Northern for SEQ. ID NO.: 8  
 NORMAL TUMOR  
 % frequency % frequency Ratios  
 N/T T/N

Bladder	0.0312	0.0460	0.6780	1.4730
Breast	0.0192	0.0282	0.6805	1.4694
Small intestine	0.0368	0.0000	undef	0.0000
Ovary	0.0210	0.0364	0.5756	1.7372
Endocrine tissue	0.0290	0.0326	0.8882	1.1258
Gastrointestinal	0.0460	0.0231	1.9880	0.5030
Brain	0.0532	0.0585	0.9094	1.0996
Hematopoietic	0.0361	0.0379	0.9528	1.0486
Skin	0.0367	0.0000	undef	0.0000
Hepatic	0.0048	0.0647	0.0735	13.5999
Heart	0.0699	0.0412	1.6961	0.5896
Testicles	0.0288	0.4210	0.0683	14.6349
Lung	0.0343	0.0368	0.9314	1.0737
Stomach-esophagus	0.0773	0.0230	3.3614	0.2975
Muscle-skeleton	0.0497	0.0660	0.7528	1.3283
Kidney	0.0353	0.1575	0.2241	4.4619
Pancreas	0.0165	0.0939	0.1760	5.6828
Penis	0.0299	0.0267	1.1232	0.8903
Prostate	0.0196	0.0298	0.6580	1.5197
Uterus-endometrium	0.0270	0.1583	0.1707	5.8579
Uterus-myometrium	0.0229	0.0679	0.3367	2.9702
Uterus-general	0.0051	0.0954	0.0534	18.7357
Breast hyperplasia	0.0192			
Prostate hyperplasia	0.0505			
Seminal vesicle	0.0890			
Sensory organs	0.0353			
White blood cells	0.0399			
Cervix	0.0319			

FETUS  
 % frequency

STANDARDIZED/SUBTRACTED  
 LIBRARIES  
 % frequency

Development	0.0417	Breast	0.0000
Gastrointestinal	0.0333	Ovary_n	0.0000
Brain	0.0313	Ovary_t	0.0152
Hematopoietic	0.0197	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0082
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0783	Hematopoietic	0.0057
Lung	0.0217	Skin-muscle	0.0032
Suprarenal gland	0.0507	Testicles	0.0077
Kidney	0.0309	Lung	0.0082
Placenta	0.0727	Nerves	0.0141
Prostate	0.0997	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0319
		Uterus_n	0.0125

09673400-122700

Electronic Northern for SEQ. ID NO.: 9

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0468	0.0204	2.2882	0.4370
Breast	0.0205	0.0451	0.4537	2.2042
Small intestine	0.0307	0.0331	0.9268	1.0739
Ovary	0.0539	0.0468	1.1511	0.8686
Endocrine tissue	0.0562	0.0527	1.0674	0.9369
Gastrointestinal	0.0249	0.0324	0.7692	1.3001
Brain	0.0333	0.0318	1.0451	0.9568
Hematopoietic	0.0388	0.0379	1.0234	0.9772
Skin	0.0257	0.1695	0.1516	6.5954
Hepatic	0.0095	0.0259	0.3676	2.7200
Heart	0.0540	0.0000	undef	0.0000
Testicles	0.0173	0.0702	0.2460	4.0652
Lung	0.0291	0.0491	0.5927	1.6872
Stomach-esophagus	0.0000	0.0230	0.0000	undef
Muscle-skeleton	0.0206	0.1140	0.1803	5.5448
Kidney	0.0733	0.0274	2.6765	0.3736
Pancreas	0.0264	0.0331	0.7977	1.2536
Penis	0.0269	0.0533	0.5054	1.9786
Prostate	0.0501	0.0341	1.4715	0.6796
Uterus-endometrium	0.0541	0.2639	0.2049	4.8816
Uterus-myometrium	0.0152	0.0611	0.2494	4.0097
Uterus-general	0.0204	0.0000	undef	0.0000
Breast hyperplasia	0.0512			
Prostate hyperplasia	0.0386			
Seminal vesicle	0.0623			
Sensory organs	0.0470			
White blood cells	0.0286			
Cervix	0.0426			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0068
Gastrointestinal	0.0557	Ovary_n	0.1595
Brain	0.0666	Ovary_t	0.0051
Hematopoietic	0.0626	Endocrine tissue	0.0245
Skin	0.0786	Fetal	0.0256
Hepatic	0.0000	Gastrointestinal	0.0732
Heart-blood vessels	0.0260	Hematopoietic	0.0057
Lung	0.0818	Skin-muscle	0.0551
Suprarenal gland	0.0867	Testicles	0.0309
Kidney	0.0761	Lung	0.0737
Placenta	0.0432	Nerves	0.0231
Prostate	0.0606	Prostate	0.0137
Sensory organs	0.0249	Sensory Organs	0.0310
	0.0628	Uterus_n	0.0333

00673400.122700

Electronic Northern for SEQ. ID NO.: 10

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.1131	0.1431	0.7900	1.2659
Breast	0.1356	0.1692	0.8015	1.2476
Small intestine	0.1962	0.0165	11.8636	0.0843
Ovary	0.1827	0.2446	0.7471	1.3385
Endocrine tissue	0.1090	0.1329	0.8202	1.2192
Gastrointestinal	0.1878	0.2590	0.7248	1.3797
Brain	0.1035	0.1325	0.7814	1.2798
Hematopoietic	0.2700	0.1894	1.4257	0.7014
Skin	0.1359	0.0847	1.6029	0.6239
Hepatic	0.0428	0.1812	0.2363	4.2311
Heart	0.2586	0.0137	18.8118	0.0532
Testicles	0.0633	0.1403	0.4510	2.2174
Lung	0.3231	0.2229	1.4495	0.6899
Stomach-esophagus	0.1643	0.2147	0.7653	1.3066
Muscle-skeleton	0.1222	0.0960	2.0524	0.4872
Kidney	0.0875	0.2328	0.5248	1.9055
Pancreas	0.1407	0.1757	0.4955	2.0183
Penis	0.1003	0.1500	0.8798	1.1366
Prostate	0.1824	0.0528	3.3080	0.7645
Uterus-endometrium	0.1677	0.3804	3.4569	0.2893
Uterus-myometrium	0.2292	0.0000	0.4409	2.2681
Uterus-general	0.0735		under	0.0000
Breast hyperplasia	0.0684			
Prostate hyperplasia	0.1335			
Seminal vesicle	0.0470			
Sensory organs	0.2749			
White blood cells	0.0958			
Cervix				

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0136
Gastrointestinal	0.0139	Ovary_n	0.3190
Brain	0.0639	Ovary_t	0.0709
Hematopoietic	0.1063	Endocrine tissue	0.0000
Skin	0.1258	Fetal	0.0326
Hepatic	0.2513	Gastrointestinal	0.1464
Heart-blood vessels	0.0260	Hematopoietic	0.0000
Lung	0.0712	Skin-muscle	0.1328
Suprarenal gland	0.1517	Testicles	0.0154
Kidney	0.0000		0.2211
Placenta	0.0988	Lung	0.0311
Prostate	0.0909	Nerves	0.0410
Sensory organs	0.1745	Prostate	0.0000
	0.0377	Sensory Organs	0.0333
		Uterus_n	

00673400.122700



Electronic Northern for SEQ. ID NO.: 11

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0156	0.0051	3.0509	0.3278
Breast	0.0064	0.0113	0.5671	1.7613
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0240	0.0234	1.0233	0.9772
Endocrine tissue	0.0068	0.0100	0.6792	1.4722
Gastrointestinal	0.0096	0.0046	2.0708	0.4829
Brain	0.0022	0.0257	0.0864	11.5747
Hematopoietic	0.0147	0.0000	undef	0.0000
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0238	0.0065	3.6765	0.2720
Heart	0.0276	0.0275	1.0023	0.9977
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0083	0.0245	0.3387	2.9526
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0086	0.0060	1.4278	0.7004
Kidney	0.0081	0.0616	0.1322	7.5658
Pancreas	0.0165	0.0000	undef	0.0000
Penis	0.0120	0.0267	0.4493	2.2259
Prostate	0.0065	0.0085	0.7677	1.3026
Uterus-endometrium	0.0270	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0951	0.0802	12.4748
Uterus-general	0.0968	0.0000	undef	0.0000
Breast hyperplasia	0.0096			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0089			
Sensory organs	0.0706			
White blood cells	0.0000			
Cervix	0.0106			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0139	Breast	0.0000
Gastrointestinal	0.0278	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0708	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0233
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0320	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0648
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0124	Lung	0.0164
Placenta	0.2121	Nerves	0.0010
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0083

00673400.122700

## Electronic Northern for SEQ. ID NO.: 12

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0351	0.3093	0.1135	8.8135
Breast	0.0269	0.0470	0.5716	1.7493
Small intestine	0.0092	0.0662	0.1390	7.1929
Ovary	0.0569	0.0182	3.1249	0.3200
Endocrine tissue	0.0528	0.0502	1.0529	0.9498
Gastrointestinal	0.0019	0.0093	0.2071	4.8289
Brain	0.0022	0.0873	0.0254	39.3541
Hematopoietic	0.0147	0.0000	undef	0.0000
Skin	0.0220	0.5085	0.0433	23.0839
Hepatic	0.0285	0.0582	0.4902	2.0400
Heart	0.0191	0.0000	undef	0.0000
Testicles	0.0115	0.0000	undef	0.0000
Lung	0.0114	0.0061	1.8629	0.5368
Stomach-esophagus	0.0193	0.0077	2.5211	0.3967
Muscle-skeleton	0.0771	0.0540	1.4278	0.7004
Kidney	0.0489	0.0137	3.5687	0.2802
Pancreas	0.0264	0.0442	0.5983	1.6714
Penis	0.0090	0.1066	0.0842	11.8713
Prostate	0.0000	0.0064	0.0000	undef
Uterus-endometrium	0.0743	0.0000	undef	0.0000
Uterus-myometrium	0.0381	0.1494	0.2551	3.9206
Uterus-general	0.0153	0.0954	0.1601	6.2452
Breast hyperplasia	0.0096			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0000			
Cervix	0.0000			

FETUS  
% frequency

Development	
Gastrointestinal	0.0696
Brain	0.4387
Hematopoietic	0.0000
Skin	0.2713
Hepatic	0.0000
Heart-blood vessels	1.6121
Lung	0.0605
Suprarenal gland	0.1770
Kidney	1.1663
Placenta	0.8092
Prostate	0.7635
Sensory organs	0.0499
	0.0000

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	0.0612
Ovary_n	0.0000
Ovary_t	0.1114
Endocrine tissue	0.0000
Fetal	0.4665
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0000
Nerves	0.0030
Prostate	0.0068
Sensory Organs	0.0000
Uterus_n	0.0291

05673400.122700

## Electronic Northern for SEQ. ID NO.: 13

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0078	0.0204	0.3814	2.6222
Small intestine	0.0256	0.0432	0.5918	1.6899
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0060	0.0078	0.7675	1.3029
Gastrointestinal	0.0000	0.0050	0.0000	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0074	0.0216	0.3428	2.9168
Skin	0.0013	0.0000	undef	0.0000
Hepatic	0.0073	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0021	0.0000	undef	0.0000
Lung	0.0115	0.0468	0.2460	4.0652
Stomach-esophagus	0.0000	0.0000	0.3810	2.6245
Muscle-skeleton	0.0580	0.0000	undef	0.0000
Kidney	0.0000	0.0300	0.0000	undef
Pancreas	0.0027	0.0000	undef	0.0000
Penis	0.0033	0.0276	0.1197	8.3871
Prostate	0.0210	0.1066	0.1966	5.0877
Uterus-endometrium	0.0022	0.0043	0.5118	1.9538
Uterus-myometrium	0.0133	0.0000	undef	0.0000
Uterus-general	0.0305	0.0883	0.3453	2.8959
Breast hyperplasia	0.0160	0.0000	undef	0.0000
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0356			
Sensory organs	0.0000			
White blood cells	0.0035			
Cervix	0.0639			

FETUS  
% frequency

Development	
Gastrointestinal	0.0000
Brain	0.0028
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0145
Suprarenal gland	0.0761
Kidney	0.0247
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	0.0408
Ovary_n	0.0000
Ovary_t	0.1266
Endocrine tissue	0.0000
Fetal	0.0047
Gastrointestinal	0.0000
Hematopoietic	0.0057
Skin-muscle	0.0032
Testicles	0.0000
Lung	0.0000
Nerves	0.0036
Prostate	0.0000
Sensory Organs	0.0208
Uterus_n	

00673400.12700  
007221.004296

Electronic Northern for SEQ. ID NO.: 14

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0195	0.0051	3.8136	0.2622
Small intestine	0.0051	0.0132	0.3889	2.5715
Ovary	0.0061	0.0000	undef	0.0000
Endocrine tissue	0.0150	0.0130	1.1513	0.8686
Gastrointestinal	0.0153	0.0150	1.0189	0.9815
Brain	0.0115	0.0000	undef	0.0000
Hematopoietic	0.0133	0.0133	0.9969	1.0031
Skin	0.0147	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	0.0000
Heart	0.0265	0.0000	0.0000	undef
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0042	0.0154	0.2540	3.9367
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0069	0.0540	0.1269	7.8795
Kidney	0.0217	0.0274	0.7930	1.2610
Pancreas	0.0165	0.0055	2.9915	0.3343
Penis	0.0090	0.0000	undef	0.0000
Prostate	0.0087	0.0170	0.5118	1.9538
Uterus-endometrium	0.0338	0.2111	0.1600	6.2484
Uterus-myometrium	0.0076	0.0475	0.1603	6.2374
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0320			
Prostate hyperplasia	0.0238			
Seminal vesicle	0.0267			
Sensory organs	0.0000			
White blood cells	0.0069			
Cervix	0.0213			

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	
Gastrointestinal	0.0417	Ovary_n	0.0068
Brain	0.0139	Ovary_t	0.0000
Hematopoietic	0.0125	Endocrine tissue	0.0051
Skin	0.0157	Fetal	0.0245
Hepatic	0.0000	Gastrointestinal	0.0035
Heart-blood vessels	0.0000	Hematopoietic	0.0244
Lung	0.0427	Skin-muscle	0.0000
Suprarenal gland	0.0253	Testicles	0.0065
Kidney	0.0000	Lung	0.0000
Placenta	0.0124	Nerves	0.0082
Prostate	0.0121	Prostate	0.0050
Sensory organs	0.0000	Sensory Organs	0.0137
	0.0126	Uterus_n	0.0155
			0.0042

03673400.122700

## Electronic Northern for SEQ. ID NO.: 15

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0078	0.0102	0.7627	1.3111
Breast	0.0026	0.0150	0.1701	5.8778
Small intestine	0.0184	0.0496	0.3707	2.6973
Ovary	0.0000	0.0052	0.0000	undef
Endocrine tissue	0.0000	0.0025	0.0000	undef
Gastrointestinal	0.0000	0.0093	0.0000	undef
Brain	0.0007	0.0072	0.1029	9.7228
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0021	0.0041	0.5080	1.9684
Stomach-esophagus	0.0000	0.0307	0.0000	undef
Muscle-skeleton	0.0086	0.0240	0.3569	2.8016
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0000	0.0055	0.0000	undef
Penis	0.0240	0.0000	undef	0.0000
Prostate	0.0065	0.0021	3.0709	0.3256
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0340	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0118			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0000
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0039	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0020
Placenta	0.0000	Nerves	0.0000
Prostate	0.0249	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0125
		Uterus_n	

002221.00422960

## Electronic Northern for SEQ. ID NO.: 16

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0153	0.2542	3.9333
Breast	0.0077	0.0038	2.0416	0.4898
Small intestine	0.0123	0.0000	undef	0.0000
Ovary	0.0060	0.0026	2.3025	0.4343
Endocrine tissue	0.0119	0.0251	0.4755	2.1032
Gastrointestinal	0.0096	0.0139	0.6903	1.4487
Brain	0.0163	0.0246	0.6600	1.5152
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0095	0.0065	1.4706	0.6800
Heart	0.0180	0.0000	undef	0.0000
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0135	0.0082	1.6511	0.6057
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0069	0.0060	1.1422	0.8755
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0033	0.0276	0.1197	8.3571
Penis	0.0090	0.0267	0.3369	2.9678
Prostate	0.0196	0.0128	1.5354	0.6513
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0408	0.0000	undef
Uterus-general	0.0357	0.0000	undef	0.0000
Breast hyperplasia	0.0128			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0267			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0375
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0071
Lung	0.0036
Suprarenal gland	0.0507
Kidney	0.0124
Placenta	0.0061
Prostate	0.0249
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0012
Gastrointestinal	0.0000
Hematopoietic	0.0097
Skin-muscle	0.0000
Testicles	0.0082
Lung	0.0050
Nerves	0.0000
Prostate	0.0000
Sensory Organs	0.0083
Uterus_n	

00673400.122700

Electronic Northern for SEQ. ID NO.: 17

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0195	0.0179	1.0896	0.9178
Breast	0.0307	0.0338	0.9074	1.1021
Small intestine	0.0184	0.0165	1.1122	0.8991
Ovary	0.0509	0.0286	1.7792	0.5620
Endocrine tissue	0.0375	0.0301	1.2453	0.8030
Gastrointestinal	0.0153	0.0093	1.6567	0.6036
Brain	0.0222	0.0452	0.4909	2.0372
Hematopoietic	0.0160	0.0000	undef	0.0000
Skin	0.0661	0.0000	undef	0.0000
Hepatic	0.0143	0.0518	0.2757	3.5266
Heart	0.0636	0.0000	undef	0.0000
Testicles	0.0173	0.0117	1.4759	0.6775
Lung	0.0177	0.0532	0.3322	3.0104
Stomach-esophagus	0.0483	0.0000	undef	0.0000
Muscle-skeleton	0.0137	0.0960	0.1428	7.0040
Kidney	0.0217	0.0685	0.3172	3.1524
Pancreas	0.0264	0.0055	4.7864	0.2089
Penis	0.0449	0.0000	undef	0.0000
Prostate	0.0283	0.0341	0.8317	1.2024
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0229	0.0679	0.3367	2.9702
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0671			
Prostate hyperplasia	0.0476			
Seminal vesicle	0.0356			
Sensory organs	0.0353			
White blood cells	0.0121			
Cervix	0.0532			

FETUS  
% frequency

Development 0.0557  
Gastrointestinal 0.0278  
Brain 0.0688  
Hematopoietic 0.0275  
Skin 0.0000  
Hepatic 0.0000  
Heart-blood vessels 0.0534  
Lung 0.0831  
Suprarenal gland 0.1014  
Kidney 0.0741  
Placenta 0.0182  
Prostate 0.1247  
Sensory organs 0.0000

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast 0.0000  
Ovary\_n 0.0000  
Ovary\_t 0.0203  
Endocrine tissue 0.0490  
Fetal 0.0169  
Gastrointestinal 0.0122  
Hematopoietic 0.0000  
Skin-muscle 0.0259  
Testicles 0.0000  
Lung 0.0082  
Nerves 0.0050  
Prostate 0.0068  
Sensory Organs 0.0000  
Uterus\_n 0.0167

002221.00442960

## Electronic Northern for SEQ. ID NO.: 18

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0195	0.0179	1.0896	0.9178
Breast	0.0371	0.0357	1.0387	0.9627
Small intestine	0.0245	0.0331	0.7415	1.3487
Ovary	0.0479	0.0390	1.2280	0.8143
Endocrine tissue	0.0356	0.0326	1.0972	0.9114
Gastrointestinal	0.0153	0.0093	1.6567	0.6036
Brain	0.0229	0.0524	0.4376	2.2951
Hematopoietic	0.0147	0.0000	undef	0.0000
Skin	0.0587	0.0000	undef	0.0000
Hepatic	0.0143	0.0518	0.2757	3.6266
Heart	0.0593	0.0000	undef	0.0000
Testicles	0.0115	0.0117	0.9839	1.0163
Lung	0.0145	0.0491	0.2964	3.3743
Stomach-esophagus	0.0290	0.0000	undef	0.0000
Muscle-skeleton	0.0120	0.1140	0.1052	9.5055
Kidney	0.0299	0.0616	0.4846	2.0634
Pancreas	0.0281	0.0055	5.0855	0.1966
Penis	0.0449	0.0000	undef	0.0000
Prostate	0.0349	0.0319	1.0919	0.9159
Uterus-endometrium	0.0203	0.0000	undef	0.0000
Uterus-myometrium	0.0152	0.0679	0.2245	4.4553
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0576			
Prostate hyperplasia	0.0446			
Seminal vesicle	0.0356			
Sensory organs	0.0235			
White blood cells	0.0130			
Cervix	0.0532			

FETUS  
% frequency

Development	0.0417
Gastrointestinal	0.0333
Brain	0.0588
Hematopoietic	0.0275
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0427
Lung	0.0957
Suprarenal gland	0.1268
Kidney	0.0741
Placenta	0.0182
Prostate	0.1247
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0253
Endocrine tissue	0.0245
Fetal	0.0326
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0518
Testicles	0.0000
Lung	0.0082
Nerves	0.0090
Prostate	0.0137
Sensory Organs	0.0000
Uterus_n	0.0208

09673400.122700



## Electronic Northern for SEQ. ID NO.: 19

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0351	0.0332	1.0561	0.9469
Small intestine	0.0269	0.0376	0.7146	1.3995
Ovary	0.0337	0.0992	0.3398	2.9425
Endocrine tissue	0.0240	0.0312	0.7675	1.3029
Gastrointestinal	0.0409	0.0075	5.4340	0.1840
Brain	0.0268	0.0971	0.2761	3.6217
Hematopoietic	0.0059	0.0113	0.5236	1.9098
Skin	0.0013	0.2273	0.0059	170.0273
Hepatic	0.0330	0.0000	undef	0.0000
Heart	0.0095	0.0388	0.2451	4.0800
Testicles	0.0223	0.0000	undef	0.0000
Lung	0.0173	0.0351	0.4920	2.0326
Stomach-esophagus	0.0395	0.0900	0.4388	2.2792
Muscle-skeleton	0.0000	0.0077	0.0000	undef
Kidney	0.0857	0.1920	0.4462	2.2413
Pancreas	0.0136	0.0205	0.6609	1.5132
Penis	0.0198	0.0221	0.8974	1.1143
Prostate	0.0629	0.0800	0.7862	1.2719
Uterus-endometrium	0.0087	0.0106	0.8189	1.2211
Uterus-myometrium	0.0676	0.0000	undef	0.0000
Uterus-general	0.0686	0.1630	0.4208	2.3761
Breast hyperplasia	0.0153	0.0000	undef	0.0000
Prostate hyperplasia	0.0735			
Seminal vesicle	0.0416			
Sensory organs	0.0000			
White blood cells	0.0235			
Cervix	0.0000	0.0426		

FETUS  
% frequency

Development	0.1113
Gastrointestinal	0.0056
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0356
Lung	0.0289
Suprarenal gland	0.0000
Kidney	0.0062
Placenta	0.1333
Prostate	0.0249
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	0.0204
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0244
Gastrointestinal	0.0000
Hematopoietic	0.0065
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0000
Nerves	0.0068
Prostate	0.0077
Sensory Organs	0.0125
Uterus_n	

09673400.122700

Electronic Northern for SEQ. ID NO.: 20

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0858	0.1048	0.8185	1.2217
Breast	0.1036	0.1729	0.5992	1.6690
Small intestine	0.1226	0.1158	1.0593	0.9441
Ovary	0.0958	0.1197	0.8009	1.2486
Endocrine tissue	0.0954	0.1128	0.8453	1.1830
Gastrointestinal	0.0900	0.1573	0.5725	1.7466
Brain	0.0658	0.0924	0.7120	1.4046
Hematopoietic	0.1109	0.0758	1.4645	0.6828
Skin	0.0918	0.0000	undef	0.0000
Hepatic	0.0333	0.0906	0.3676	2.7200
Heart	0.2120	0.0412	5.1398	0.1946
Testicles	0.0690	0.3625	0.1904	5.2509
Lung	0.0696	0.1186	0.5869	1.7040
Stomach-esophagus	0.0483	0.0460	1.0504	0.9520
Muscle-skeleton	0.0702	0.2820	0.2491	4.0145
Kidney	0.0652	0.1027	0.6344	1.5762
Pancreas	0.1140	0.1270	0.8974	1.1143
Penis	0.1018	0.0000	undef	0.0000
Prostate	0.1090	0.1277	0.8530	1.1723
Uterus-endometrium	0.1149	0.0000	undef	0.0000
Uterus-myometrium	0.0686	0.2106	0.3258	3.0692
Uterus-general	0.0458	0.1908	0.2402	4.1635
Breast hyperplasia	0.1279			
Prostate hyperplasia	0.1159			
Seminal vesicle	0.1157			
Sensory organs	0.1059			
White blood cells	0.0832			
Cervix	0.1278			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0136
Gastrointestinal		Ovary_n	0.1595
Brain	0.0557	Ovary_t	0.0658
Hematopoietic	0.2471	Endocrine tissue	0.0000
Skin	0.2189	Fetal	0.0216
Hepatic	0.1612	Gastrointestinal	0.0732
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.1560	Skin-muscle	0.0259
Suprarenal gland	0.2633	Testicles	0.0000
Kidney	0.1012	Lung	0.1638
Placenta	0.1014	Nerves	0.0211
Prostate	0.1112	Prostate	0.0205
Sensory organs	0.0848	Sensory Organs	0.0000
	0.3740	Uterus_n	0.0333
	0.0126		

00673400.122700

NORMAL	TUMOR	Ratios
% frequency	% frequency	N/T

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0204
Gastrointestinal		Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0101
Hematopoietic	0.0111	Endocrine tissue	0.0490
Skin	0.0000	Fetal	0.0093
Hepatic	0.0157	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0421
Suprarenal gland	0.0107	Testicles	0.0154
Kidney	0.0000	Lung	0.0000
Placenta	0.0247	Nerves	0.0010
Prostate	0.0000	Prostate	0.0274
Sensory organs	0.0000	Sensory Organs	0.0000
	0.0000		0.0000

Electronic Northern for SEQ. ID NO.: 22

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0000	0.0102	0.0000 undef	
Small intestine	0.0064	0.0207	0.3093 3.2328	
Ovary	0.0153	0.0662	0.2317 4.3157	
Endocrine tissue	0.0180	0.0156	1.1513 0.8686	
Gastrointestinal	0.0204	0.0351	0.5822 1.7176	
Brain	0.0153	0.0231	0.6627 1.5090	
Hematopoietic	0.0510	0.0257	1.9871 0.5032	
Skin	0.0134	0.0000	undef 0.0000	
Hepatic	0.0367	0.0000	undef 0.0000	
Heart	0.0095	0.0000	undef 0.0000	
Testicles	0.0456	0.0000	undef 0.0000	
Lung	0.0000	0.0117	0.0000 undef	
Stomach-esophagus	0.0249	0.0348	0.7172 1.3943	
Muscle-skeleton	0.0193	0.0077	2.5211 0.3967	
Kidney	0.0377	0.0300	1.2564 0.7959	
Pancreas	0.0244	0.0274	0.8922 1.1209	
Penis	0.0083	0.0166	0.4986 2.0057	
Prostate	0.0329	0.0267	1.2355 0.8094	
Uterus-endometrium	0.0131	0.0149	0.8774 1.1397	
Uterus-myometrium	0.0338	0.0000	undef 0.0000	
Uterus-general	0.0000	0.0340	0.0000 undef	
Breast hyperplasia	0.0153	0.0000	undef 0.0000	
Prostate hyperplasia	0.0256			
Seminal vesicle	0.0238			
Sensory organs	0.0000			
White blood cells	0.0069			
Cervix	0.0213			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0000
Gastrointestinal	0.0139	Ovary_n	0.3190
Brain	0.0194	Ovary_t	0.0000
Hematopoietic	0.0125	Endocrine tissue	0.0000
Skin	0.0039	Fetal	0.0373
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0114
Lung	0.0320	Skin-muscle	0.0680
Suprarenal gland	0.0434	Testicles	0.0231
Kidney	0.0000	Lung	0.0000
Placenta	0.0124	Nerves	0.0211
Prostate	0.0061	Prostate	0.0205
Sensory organs	0.0000	Sensory Organs	0.0077
	0.0251	Uterus_n	0.0458

002221.00422600

Electronic Northern for SEQ. ID NO.: 23

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0741	0.0639	1.1593	0.8626
Breast	0.0691	0.0827	0.8352	1.1973
Small intestine	0.0245	0.0496	0.4943	2.0230
Ovary	0.0689	0.0494	1.3936	0.7176
Endocrine tissue	0.2487	0.5191	0.4791	2.0873
Gastrointestinal	0.0421	0.0879	0.4796	2.0852
Brain	0.1700	0.1037	1.6395	0.6099
Hematopoietic	0.0695	0.0758	0.9175	1.0899
Skin	0.0367	0.4237	0.0866	11.5419
Hepatic	0.0143	0.0388	0.3676	2.7200
Heart	0.0668	0.1375	0.4857	2.0588
Testicles	0.0460	0.0468	0.9839	1.0163
Lung	0.0592	0.0470	1.2590	0.7943
Stomach-esophagus	0.1160	0.0690	1.6807	0.5950
Muscle-skeleton	0.0754	0.0960	0.7853	1.2735
Kidney	0.0706	0.0479	1.4728	0.6790
Pancreas	0.0677	0.0552	1.2265	0.8153
Penis	0.0988	0.0267	3.7064	0.2698
Prostate	0.0697	0.0660	1.0566	0.9464
Uterus-endometrium	0.0608	0.0000	undef	0.0000
Uterus-myometrium	0.0152	0.0611	0.2494	4.0097
Uterus-general	0.1120	0.0000	undef	0.0000
	0.0480			
Breast hyperplasia		0.0565		
Prostate hyperplasia		0.0445		
Seminal vesicle		0.0823		
Sensory organs		0.0824		
White blood cells		0.0852		
Cervix				

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0544
Gastrointestinal	0.1113	Ovary_n	0.0000
Brain	0.0805	Ovary_t	0.0203
Hematopoietic	0.1376	Endocrine tissue	0.0245
Skin	0.1140	Fetal	0.0309
Hepatic	0.0000	Gastrointestinal	0.0610
Heart-blood vessels	0.0520	Hematopoietic	0.0000
Lung	0.0996	Skin-muscle	0.0356
Suprarenal gland	0.1951	Testicles	0.0077
Kidney	0.1268	Lung	0.0655
Placenta	0.1359	Nerves	0.0793
Prostate	0.1030	Prostate	0.0547
Sensory organs	0.0748	Sensory Organs	0.0000
	0.0879	Uterus_n	0.0063

00227 004290

Electronic Northern for SEQ. ID NO.: 24

	NORMAL	TUMOR	Ratios	T/N
	% frequency	% frequency	N/T	
Bladder	0.0546	0.0332	1.6428	0.6087
Breast	0.0269	0.0320	0.8407	1.1896
Small intestine	0.0276	0.0000	undef	0.0000
Ovary	0.0479	0.0546	0.8771	1.1401
Endocrine tissue	0.0324	0.0176	1.8437	0.5424
Gastrointestinal	0.0211	0.0463	0.4556	2.1950
Brain	0.0229	0.0277	0.8266	1.2097
Hematopoietic	0.0348	0.0379	0.9175	1.0899
Skin	0.0184	0.0000	undef	0.0000
Hepatic	0.0190	0.0000	undef	0.0000
Heart	0.0477	0.0000	undef	0.0000
Testicles	0.0230	0.1159	0.1968	5.0816
Lung	0.0156	0.0307	0.5080	1.9684
Stomach-esophagus	0.0000	0.0460	0.0000	undef
Muscle-skeleton	0.0120	0.0480	0.2499	4.0023
Kidney	0.0163	0.0068	2.3791	0.4203
Pancreas	0.0182	0.0331	0.5484	1.8234
Penis	0.0180	0.0900	0.2246	4.4517
Prostate	0.0174	0.0170	1.0236	0.9769
Uterus-endometrium	0.0541	0.0000	undef	0.0000
Uterus-myometrium	0.0229	0.0579	0.3367	2.9702
Uterus-general	0.0102	0.0000	undef	0.0000
Breast hyperplasia	0.0576			
Prostate hyperplasia	0.0208			
Seminal vesicle	0.0089			
Sensory organs	0.0118			
White blood cells	0.0277			
Cervix	0.0213			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0000
Gastrointestinal	0.0278	Ovary_n	0.0000
Brain	0.0639	Ovary_t	0.0000
Hematopoietic	0.0438	Endocrine tissue	0.0000
Skin	0.0275	Fetal	0.0006
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0825	Skin-muscle	0.0000
Suprarenal gland	0.0831	Testicles	0.0077
Kidney	0.0000	Lung	0.0000
Placenta	0.0803	Nerves	0.0040
Prostate	0.0657	Prostate	0.0000
Sensory organs	0.0249	Sensory Organs	0.0000
	0.0000	Uterus_n	0.0000

09873400.122700

## Electronic Northern for SEQ. ID NO.: 25

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0429	0.0486	0.8832	1.1323
Breast	0.0435	0.0771	0.5643	1.7720
Small intestine	0.0307	0.0000	undef	0.0000
Ovary	0.0389	0.0833	0.4677	2.1381
Endocrine tissue	0.0460	0.0301	1.5283	0.6543
Gastrointestinal	0.0287	0.0971	0.2958	3.3803
Brain	0.0347	0.0534	0.6507	1.5367
Hematopoietic	0.0869	0.0000	undef	0.0000
Skin	0.0551	0.0947	0.6498	1.5389
Hepatic	0.0143	0.0194	0.7353	1.3600
Heart	0.0466	0.0137	3.3923	0.2946
Testicles	0.0173	0.0935	0.1845	5.4203
Lung	0.0457	0.0613	0.7451	1.3421
Stomach-esophagus	0.0290	0.0153	1.8908	0.5289
Muscle-skeleton	0.0223	0.1140	0.1954	5.1183
Kidney	0.0407	0.0137	2.9739	0.3363
Pancreas	0.0314	0.0442	0.7105	1.4075
Penis	0.0779	0.0533	1.4601	0.6849
Prostate	0.0458	0.0617	0.7412	1.3491
Uterus-endometrium	0.0473	0.0000	undef	0.0000
Uterus-myometrium	0.0305	0.1087	0.2806	3.5642
Uterus-general	0.0357	0.0954	0.3736	2.6765
Breast hyperplasia	0.0256			
Prostate hyperplasia	0.0803			
Seminal vesicle	0.0801			
Sensory organs	0.0118			
White blood cells	0.0494			
Cervix	0.0426			

FETUS  
% frequency

Development	
Gastrointestinal	0.0417
Brain	0.0611
Hematopoietic	0.0626
Skin	0.0708
Hepatic	0.0000
Heart-blood vessels	0.0260
Lung	0.0534
Suprarenal gland	0.0542
Kidney	0.0761
Placenta	0.0988
Prostate	0.0303
Sensory organs	0.0000
	0.0251

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	0.0204
Ovary_n	0.1595
Ovary_t	0.0101
Endocrine tissue	0.0000
Fetal	0.0132
Gastrointestinal	0.0000
Hematopoietic	0.0194
Skin-muscle	0.0077
Testicles	0.0328
Lung	0.0161
Nerves	0.0068
Prostate	0.0000
Sensory Organs	0.0291
Uterus_n	

09673400.122700

Electronic Northern for SEQ. ID NO.: 26  
 NORMAL TUMOR  
 % frequency % frequency N/T T/N

Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	3.0675	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0015	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0340	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
 % frequency

STANDARDIZED/SUBTRACTED  
 LIBRARIES  
 % frequency

Development	
Gastrointestinal	0.0000
Brain	0.0028
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0061
Sensory organs	0.0000
	0.0000

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0070
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0000
Nerves	0.0000
Prostate	0.0155
Sensory Organs	0.0250
Uterus_n	

002327.0045296



## Electronic Northern for SEQ. ID NO.: 27

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0230	0.1695	5.8999
Breast	0.0179	0.0395	0.4537	2.2042
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0300	0.0130	2.3025	0.4343
Endocrine tissue	0.0068	0.0251	0.2717	3.6805
Gastrointestinal	0.0077	0.0093	0.8283	1.2072
Brain	0.0015	0.0092	0.1600	6.2504
Hematopoietic	0.0053	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0194	0.0000	undef
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0083	0.0368	0.2258	4.4288
Stomach-esophagus	0.0290	0.0230	1.2603	0.7933
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0136	0.0068	1.9825	0.5044
Pancreas	0.0000	0.0276	0.0000	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0065	0.0128	0.5118	1.9538
Uterus-endometrium	0.0473	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0340	0.0000	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0213			

FETUS  
% frequency

Development	
Gastrointestinal	0.0139
Brain	0.0278
Hematopoietic	0.0125
Skin	0.0079
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0320
Suprarenal gland	0.0289
Kidney	0.0000
Placenta	0.0185
Prostate	0.0000
Sensory organs	0.0997
	0.0000

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0304
Fetal	0.0245
Gastrointestinal	0.0029
Hematopoietic	0.0122
Skin-muscle	0.0114
Testicles	0.0097
Lung	0.0000
Nerves	0.0164
Prostate	0.0020
Sensory Organs	0.0068
Uterus_n	0.0000
	0.0000

00221\*0043\*960

## Electronic Northern for SEQ. ID NO.: 28

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0195	0.0383	0.5085	1.9666
Breast	0.0256	0.0714	0.3582	2.7919
Small intestine	0.0552	0.0331	1.6683	0.5994
Ovary	0.0270	0.0468	0.5756	1.7372
Endocrine tissue	0.0477	0.0451	1.0566	0.9464
Gastrointestinal	0.0326	0.0324	1.0058	0.9942
Brain	0.0503	0.0277	1.8132	0.5515
Hematopoietic	0.0201	0.1894	0.1059	9.4460
Skin	0.0367	0.2542	0.1444	6.9252
Hepatic	0.0476	0.0388	1.2255	0.8160
Heart	0.0699	0.0550	1.2721	0.7861
Testicles	0.0173	0.1403	0.1230	8.1305
Lung	0.0395	0.0818	0.4826	2.0720
Stomach-esophagus	0.0676	0.0613	1.1030	0.9065
Muscle-skeleton	0.0394	0.0300	1.3135	0.7613
Kidney	0.0462	0.0616	0.7490	1.3351
Pancreas	0.0347	0.0607	0.5711	1.7510
Penis	0.0509	0.1600	0.3182	3.1424
Prostate	0.0327	0.0149	2.1935	0.4559
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0076	0.0543	0.1403	7.1284
Uterus-general	0.0357	0.0000	undef	0.0000
Breast hyperplasia	0.0192			
Prostate hyperplasia	0.0565			
Seminal vesicle	0.0445			
Sensory organs	0.0941			
White blood cells	0.0390			
Cervix	0.0319			

FETUS  
% frequency

Development	
Gastrointestinal	0.0537
Brain	0.0194
Hematopoietic	0.0188
Skin	0.0197
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0320
Suprarenal gland	0.0325
Kidney	0.0000
Placenta	0.0371
Prostate	0.0242
Sensory organs	0.0997
	0.0000

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	0.0340
Ovary_n	0.0000
Ovary_t	0.0101
Endocrine tissue	0.0000
Fetal	0.0396
Gastrointestinal	0.0244
Hematopoietic	0.0000
Skin-muscle	0.0778
Testicles	0.0000
Lung	0.0000
Nerves	0.0231
Prostate	0.0479
Sensory Organs	0.0697
Uterus_n	0.0291

09673400.122700

Electronic Northern for SEQ. ID NO.: 29

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0663	0.0358	1.8523	0.5399
Breast	0.0512	0.0489	1.0470	0.9551
Small intestine	0.0368	0.0496	0.7415	1.3487
Ovary	0.0779	0.0728	1.0690	0.9354
Endocrine tissue	0.0562	0.0326	1.7242	0.5800
Gastrointestinal	0.0345	0.0370	0.9319	1.0731
Brain	0.0392	0.0524	0.7482	1.3366
Hematopoietic	0.0602	0.0379	1.5880	0.6297
Skin	0.0587	0.0000	undef	0.0000
Hepatic	0.0095	0.0647	0.1471	6.7999
Heart	0.0583	0.0550	1.0601	0.9433
Testicles	0.0173	0.1520	0.1135	8.8080
Lung	0.0208	0.0491	0.4234	2.3620
Stomach-esophagus	0.0387	0.0460	0.8404	1.1900
Muscle-skeleton	0.0360	0.0420	0.8567	1.1673
Kidney	0.0380	0.0616	0.6168	1.6213
Pancreas	0.0314	0.0884	0.3552	2.8150
Penis	0.0689	0.0267	2.5833	0.3871
Prostate	0.0436	0.0490	0.8901	1.1235
Uterus-endometrium	0.0541	0.0000	undef	0.0000
Uterus-myometrium	0.0381	0.1155	0.3301	3.0296
Uterus-general	0.0815	0.0000	undef	0.0000
Breast hyperplasia	0.0831			
Prostate hyperplasia	0.0446			
Seminal vesicle	0.0801			
Sensory organs	0.0353			
White blood cells	0.0520			
Cervix	0.0532			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development  
Gastrointestinal  
Brain  
Hematopoietic  
Skin  
Hepatic  
Heart-blood vessels  
Lung  
Suprarenal gland  
Kidney  
Placenta  
Prostate  
Sensory organs

0.0000  
0.0389  
0.0188  
0.0472  
0.0000  
0.0260  
0.0498  
0.0614  
0.0254  
0.0741  
0.0364  
0.0499  
0.0000

Breast  
Ovary\_n  
Ovary\_t  
Endocrine tissue  
Fetal  
Gastrointestinal  
Hematopoietic  
Skin-muscle  
Testicles  
Lung  
Nerves  
Prostate  
Sensory Organs  
Uterus\_n

0.0000  
0.1595  
0.0203  
0.0000  
0.0093  
0.0366  
0.0000  
0.0130  
0.0000  
0.0164  
0.0120  
0.0205  
0.0000  
0.0208

002221.0042960

Electronic Northern for SEQ. ID NO.: 30

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0078	0.0000	undef	0.0000
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0092	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0034	0.0000	undef	0.0000
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0011	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0010	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0109	0.0021	5.1181	0.1954
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0340	0.0000	undef
Uterus-myometrium	0.0102	0.0000	undef	0.0000
Uterus-general	0.0000			
Breast hyperplasia	0.0039			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells				
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

00673400.122700

Electronic Northern for SEQ. ID NO.: 31

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0051	0.0000	undef
Breast	0.0038	0.0019	2.0416	0.4899
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0030	0.0104	0.2879	3.4745
Endocrine tissue	0.0034	0.0100	0.3396	2.9444
Gastrointestinal	0.0057	0.0046	1.2425	0.8048
Brain	0.0111	0.0051	2.1599	0.4530
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0095	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0042	0.0102	0.4064	2.4605
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0060	0.5711	1.7510
Kidney	0.0163	0.0068	2.3791	0.4203
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0090	0.0000	undef	0.0000
Prostate	0.0022	0.0021	1.0236	0.9769
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0340	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0024	0.0030		
Prostate hyperplasia	0.0089	0.0000		
Seminal vesicle	0.0000	0.0000		
Sensory organs	0.0061	0.0213		
White blood cells				
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0028	Ovary_t	0.0000
Hematopoietic	0.0125	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0036	Testicles	0.0000
Kidney	0.0062	Lung	0.0082
Placenta	0.0303	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0126	Sensory Organs	0.0000
		Uterus_n	0.0000

00673400.122700

Electronic Northern for Seq. ID: 52

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma			
Bladder			
Breast	0.0599	0.0543	1.1037 0.9060
Large intestine	0.0507	0.0282	1.7979 0.5562
Small intestine	0.0326	0.0450	0.7240 1.3811
Ovary	0.0268	0.0113	0.8563 1.1679
Endocrine tissue	0.0419	0.0426	1.0306 0.9703
Brain	0.0564	0.0453	1.2443 0.8017
Skin	0.0642	0.0510	1.2113 0.8255
Hepatic	0.0380	0.0379	1.0022 0.9978
Heart	0.0330	0.0789	0.4190 2.3868
Testicles	0.0093	0.0508	0.1831 5.4614
Lung	0.0589	0.0000	undef 0.0000
Stomach-esophagus	0.0482	0.0533	0.9047 1.1054
Muscle-skeleton	0.0389	0.0499	0.7796 1.2828
Kidney	0.0072	0.0256	0.2813 3.5296
Pancreas	0.0240	0.0702	0.3418 2.9256
Prostate	0.0694	0.0289	2.3984 0.4169
T lymphoma	0.0297	0.0331	0.8974 1.1143
Uterus	0.0443	0.0287	1.5457 0.6470
White blood cells	0.0505	0.1643	0.3074 3.2533
Hematopoietic	0.0325	0.0690	0.4715 2.1210
Penis	0.0363	0.0304	1.1948 0.8370
Seminal vesicle	0.0495		
Sensory organs	0.0322		
	0.0470		

FETUS  
% freq.

Development	0.0695
Gastrointestinal	0.0750
Brain	0.0876
Hematopoietic	0.0904
Skin	0.0000
Hepatic	0.0260
Heart-blood vessels	0.0854
Lung	0.0267
Adrenal gland	0.0761
Kidney	0.0556
Placenta	0.0606
Prostate	0.0499
Sensory organs	0.0628

STANDARDIZED/SUBTRACTED LIBRARIES  
% frequency

Breast	0.0068
Breast t	0.0000
Large Intestine t	0.0000
Ovary n	0.1595
Ovary t	0.0101
Endocrine tissue	0.0245
Fetal	0.0294
Gastrointestinal	0.0732
Hematopoietic	0.0000
Skin-muscle	0.0616
Testicles n	0.0293
Testicles t	0.0000
Lungs n	0.0195
Lungs t	0.0000
Nerves	0.0261
Kidney t	0.0000
Ovary uterus	0.0293
Prostate n	0.0121
Sensory organs	0.0310
White blood cells	0.0000

002221.00427360

## 2.2. Fisher Test

In order to decide whether a partial sequence *S* of a gene occurs significantly more often or less often in a library for normal tissue than in a library for degenerated tissue, Fisher's exact test, a standard statistical process, is carried out (Hays, W. L., (1991) Statistics, Harcourt Brace College Publishers, Fort Worth).

The null hypothesis reads: The two libraries cannot be distinguished with respect to the frequency of sequences homologous to *S*. If the null hypothesis can be rejected with high enough certainty, the gene belonging to *S* is accepted as an advantageous candidate for a cancer gene, and in the next step an attempt is made to achieve lengthening of its sequence.

### Example 3

#### Automatic Lengthening of the Partial Sequence

Automatic lengthening of partial sequence *S* is completed in three steps:

1. Determination of all sequences homologous to *S* from the total set of available sequences using BLAST
2. Assembling these sequences by means of the standard program GAP4 (Bonfield, J. K.; Smith, K. F. and Staden, R. (1995), Nucleic Acids Research 23 4992-4999) (contig formation).
3. Computation of a consensus sequence *C* from the assembled sequences.

Consensus sequence *C* will generally be longer than initial sequence *S*. Its electronic Northern Blot will accordingly

00673400122700

deviate from that for S. A repeated Fisher test decides whether the alternative hypothesis of deviation from a uniform expression in the two libraries can be maintained. If this is the case, an attempt is made to lengthen C in the same way as S. This iteration is continued with consensus sequences  $C_i$  ( $i$ : iteration index) obtained in each case until the alternative hypothesis is rejected (if  $H_0$  Exit; truncation criterion I) or until automatic lengthening is no longer possible (while  $C_i > C_{i-1}$ ; truncation criterion II).

In the case of truncation criterion II, with the consensus sequence present after the last iteration, a complete or roughly complete sequence of a gene which can be related to cancer with high statistical certainty is acquired.

Analogously to the above-described examples, it was possible to find from hystero myomic tissue the nucleic acid sequences described in Table I.

Furthermore, for the individual nucleic acid sequences, it was possible to determine the peptide sequences (ORF's) that are listed in Table II, in which no peptide can be assigned to a few nucleic acid sequences and more than one peptide can be assigned to some nucleic acid sequences. As already mentioned above, both the determined nucleic acid sequences and the peptide sequences assigned to the nucleic acid sequences are the subject of this invention.

09673400.122700



**Example 4****Mapping of Nucleic Acid Sequences on the Human Genome**

Human genes were mapped using the Stanford G3 Hybrid Panel (Stewart et al., 1997), which is marketed by Research Genetics, Huntsville, Alabama. This panel consists of 83 different genomic DNAs of human-hamster hybrid cell lines and allows resolution of 500 kilobases. The hybrid cell lines were obtained by fusion of irradiated diploid human cells with cells of the Chinese hamster. The retention pattern of the human chromosome fragments is determined by means of gene-specific primers in a polymerase chain reaction and is analyzed using software available from the Stanford RH server ([http://www.stanford.edu/RH/rhserver\\_form2.html](http://www.stanford.edu/RH/rhserver_form2.html)). This program determines the STS marker that is nearest to the desired gene. The corresponding cytogenetic band was determined using the "Mapview" program of the Genome Database (GDB), (<http://gdbwww.dkfz-heidelberg.de>).

In addition to mapping of genes on the human chromosome set by various experimental methods, it is possible to determine the location of genes on this by biocomputer methods. To do this, the known program e-PCR was used (Schuler GD (1998) Electronic PCR: Bridging the Gap between Genome Mapping and Genome Sequencing. Trends Biotechnol 16: 456-459, Schuler GD (1997). Sequence Mapping by Electronic PCR. Genome Res. 7: 541-550). The database used here no longer corresponds to the one cited in the literature, but is a further development which includes data from the public database RHdb (<http://www.ebi.ac.uk/RHdb/-index.html>). Analogously to the mapping by the hybrid panels,

00573400-122700

the results were evaluated with the above-mentioned software and the software of the Whitehead Institute  
(<http://carbon.wi.mit.edu:8000/cgi-bin/contig/rhmapper.pl>).

09673400-122700

Col. 1 - Sequence ID No.:

Col. 2 - Expression in hysteromyomic tissue:

Col. 3 - Function

Col. 4 - Modules

Col. 5 - Length of the applied sequence in bases

Col. 6 - Cytogenetic localization

Col. 7 - Next marker

[Key to Table I:]

[Col. 2:] erhöht = elevated

[Col. 3:]

[Seq. ID No.: 14, 15, 17, 30, 31] unbekannt = unknown

[Seq. ID No.: 16] Homolog zu Homo sapiens... = homologous  
to homo sapiens...

[Seq. ID No.: 18] Humanes Homolog zu ... = human homolog to

[Seq. ID No.: 52] Verlängerung von Seq. ID. 14 =  
Lengthening of Seq. ID. 14

TABLE I

Sequenz ID No.:	Expression im Uterus-Myogewebe:	Funktion	Module	Länge der angemeindeten Sequenz in Basen	Cytogenetische Lokalisation	nächster Marker
1	erhöht	Human mRNA for ornithine decarboxylase antizymo	"alhydro-lase"	779		
2	erhöht	Human MEST mRNA		2310		
3	erhöht	Human cocaine and amphetamine regulated transcript CART (ICART)		864	5q11.2-q13.1	D5S1730
4	erhöht	Human microfilament-associated glycoprotein (MFAP2)		1112	1p36.11-p36.13	
5	erhöht	Human mRNA for KIAA008 gene	"kazal"	1051	2p23.3	D2S387
6	erhöht	Human SPARC/osteonectin	"rnm"	1616	5p32-q33.1	
7	erhöht	Human sapiens splicing factor, arginine/serine-rich 7 (SFRS7)		2367	2p22.3-p22.1	WI-9798
8	erhöht	Human diacylglycerol kinase	3x "TIM"	568		
9	erhöht	Human nuclear ribonucleoprotein particle (hnRNP) C	"Thymosin"	1775		
10	erhöht	Human thymosin beta-4	"IGFBP"	509		
11	erhöht	Human growth hormone-dependent insulin-like growth factor-binding protein mRNA	thyro globulin, 1"	2191	7p12.2 p13	
12	erhöht	Human H19		1769		
13	erhöht	Human cellular retinoic acid-binding protein II (CRABP)	"lipocalin"	1026		
14	erhöht	unbekannt	"rnm"	876	14p11.2-14p11.1	WI-4204
15	erhöht	unbekannt		1284		
16	erhöht	Homolog zu Homo sapiens mRNA for putatively prenylated protein		537		
17	erhöht	unbekannt		823		
18	erhöht	Human homolog zu P. vivax pva1 gene		1002		
19	erhöht	Human laminin mRNA	5x "LR"	1548	12q21.31-12q21.33	D12S351
20	erhöht	Human 37 kD laminin receptor precursor/p40 ribosome associated protein	"S2"	844		
21	erhöht	Human YMP	"PMMP22"	862		
22	erhöht	Human NADH ubiquinone oxidoreductase M1 RQ subunit		546		
23	erhöht	Human mRNA for coupling protein G(s) alpha-subunit	"G-alpha", "aif"	1591	20q13.32-q13.33	
24	erhöht	Human hnRNP core protein A1	"rnm"	441		
25	erhöht	Human HMG-17 gene for non histone chromosomal protein	"HMG14_17"	1131		
26	erhöht	H sapiens mRNA for prolactin (clone PRL 205)	"hormone"	1071		
27	erhöht	Human mRNA for neurite outgrowth-promoting protein.	3x "PTN MK"	896		
28	erhöht	H sapiens mRNA for proliferation-associated gene (pap)	"AipC-TSA"	1050	1p32.3-p34.3	
29	erhöht	H sapiens alpha MAC		581		
30	erhöht	unbekannt		284		
31	erhöht	unbekannt		111		
62	erhöht	Verlängerung von Seq. ID. 14	"rnm"	3665	14p11.2-14p11.1	WI-4204

# References to the modules:

Pfam: Protein families database of alignments and HMMs  
(pfam@sanger.ac.uk)

PROSITE: The PROSITE database, its status in 1999. Nucleic  
Acids Res. 27: 215-219 (<http://www.expasy.ch/sprot/prosite.html>)

09673400.122700

TABLE II

## DNA Sequences

Seq. ID. No.

14

15

16

17

18

30

31

52

## Peptide Sequences (ORF's)

Seq. ID. No.

32

33

34

35

36

37

38

39

40

41

42

43

44

45

46

47

48

49

50

51

53

54

55

0673400.12200

The inventive nucleic acid sequences Seq. ID No. 1 to Seq. ID No. 31 of the determined candidate genes and the determined amino acid sequences Seq. ID No. 32 to Seq. ID No. 51 are described in the following sequence protocol.

## Sequence Protocol

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: metaGen - Gesellschaft für Genomforschung  
mbH  
(B) STREET: Innestrasse 63  
(C) CITY: Berlin  
(E) COUNTRY: Germany  
(F) POSTAL CODE (ZIP): D-14195  
(G) TELEPHONE: (030)-8413 1673  
(H) FAX: (030)-8413 1674

(ii) TITLE OF INVENTION: Human Nucleic Acid Sequences from  
Hysteromyomic Tissue

(iii) Number of sequences: 55

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: Patentin release #1.0, version #1.25  
(EPO)

## (2) INFORMATION ON SEQ ID NO. 1:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 779 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

agcgaacgacg ggcggcgggcg cggagagacg cagcggagggt ttctctgggt tcggacccca 60  
 gcggccggat ggtgaaatcc tccctgcagc ggatcctcaa tagccactgc ttcgccagag120  
 agaaggaagg ggataaaacc agcggccacca tccacgccag ccgcaccatg ccgctccta180  
 gcctgcacag ccgcggcgcc agcagcagtg agagtctccag ggtctccctc cactgctgta240  
 gtaacccggg tccggggcct cgggtgggtct cctgatgcc ctcacccacc cctgaagatc300  
 ccagggtggc gaggggaatg tcaaaaggac cacaatcttt cagctaaatt attctactcc360  
 gatgatcggc tgaatgtaac agaggaaacta acgtccaacg acaagacgag gattctcaac420  
 gtccagatcca ggctcacaga cgccaaacgc attactggc gaacagtgct gagtggcggc480  
 actgctctac atcgagatcc cgggcggcg cgtgcccag gggagcaagg acagctttgc540  
 agttctctcg ggaattcgct gaggagcagc tgcgagggcg accatgtctt aatttgccttc600  
 cacaagaacc ccgaggacag agccgccttg ctccgaacct tcagcttttt cgggcttgag660  
 attttgagac cggggcatcc cctttgttcc ccaagagacc cgacgcttgc ttcattgggccc720  
 tacaagtctc gaggagagat ctttggggag aggaagaagg attagggggc gcgtcgggt 779

## (2) INFORMATION ON SEQ ID NO. 2:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 2310 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

00673400-12700



(vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:

(vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

gtcttcacgaa acatggagtc ctgtaggcaa gctcttacct gaatcaggat gaggggagctgg 60  
 tgggtccagg tggggctgct ggccgtgccc ctgcttgctg cgtacctgca catcccaccc 120  
 cctcagcgct ccctcgccct tcaactcatgg aagtcttcag gcaagttttt cacttacaagg 180  
 ggaactgcgt tcttctacca agactctgtg ggtgtgggtg gaaagtcaga gatagtgtgtg 240  
 cttttacacg gttttccaac atccagctac gactggcaca agatttggga aggtctgacc 300  
 ttgaggtttc atcggtgat tgccttgat ttcttaggt ttggcttcag tcacaaaaccg 360  
 agacccatc actattccat atttgagcag gccagcatcg tgggaagcgt tttgcccgat 420  
 ctggggcttc agaaccgcag gatcaacott ctcttcacg actatggaga tattgttgtc 480  
 caggagcttc tctacaggt caagcagaat cgtctctgct ggcttaccat aaagagcttc 540  
 tgtctgtcaa atggagggtat ctttccctgag actcaccgct cactccctct ccaaaagcta 600  
 ctcaaaagat gagggtgtct gtcacccatc ctccacagac tgatgaactt cttgtattcc 660  
 tctcgaggtc tcaccccagt ctttgggccc tatactcggc cctctgagag tgagctgtgtg 720  
 gacatgtggg cagggatccg caacaatgac ggggaacttag tcatggacag tctcttcacg 780

tacatcaatc agaggaagaa gttcagaagg cgctgtgg gagctcttgc cttctgaact 840  
 atccccatcc atttatacta tggggccattg gatcccca atccccatcc agagtttttg 900  
 gagctgtaca ggaaaacgct gcgcgggtcc acagtgaga tcttggtatga ccacattagc 960  
 cactatccac agctagagga tcccatgggc ttcttgaaat catatatggg cttcatcaac1020  
 tcttctgtag ctggaagag tagcttccct gtattaccct cctactcccc ttatgtgttg1080  
 tgtattccac ttggaagaaa atgccccaaa gaggctcctgg ccatcaaaac taattctctc1140  
 acaaaagtcca ctttactcaa attggtgaac agtgtatagg aagaagccag caggagctct1200  
 gactaaggtt gacataatag tccacctccc attactttga tatctgatca aatgtataga1260  
 cttggctttg ttttttgtgc tattaggaaa ttctgatgag cattactatt cactgtatga1320  
 gaaagacgct cttttgcata aaagactttt ttaaacactt tggactcttc tgaataattt1380  
 agaaagtgtc atttctggcc caccoccaac aggaattcta tagtaagggg gaggagaagg1440  
 ggggctctct cctctccttc gaatgacgtt atgggcacat gcccttttaa agttctttaa1500  
 gcaacacaga gctgagtcct ctttgccata cctttggatt tagtgtttca tcaagctgtt1560  
 ttagtataaa acatttttgt aaaatagata ttggtttaaa tgatacagta ttttaggtat1620  
 gatttaagac tatgtattac ctatacatta tatatatatt ataaaagatac taaaccagca1680  
 tacccttact ctgcccagagt agtgaagcta attaaacacg tttgtttctt gaataaattg1740  
 aactaaatcc aaactatttc ctaaaatcac aggaacattaa ggaaccaatag catctgtggc1800  
 agagatgtag tgttatttag tgggaagacc aattcttaac gcaaatatac gtctgagact1860  
 cctcatacct cagtggttag aagcatgtct cctctgagct acagtagagg ggaagggatt1920  
 gtgtgttagt caagtaccca tgcgtgaatg acactgatct ctttatgatg acctgttaac1980  
 tccccactgc ctgtcccgaga gaggctttcc aatgtagctc agtaattcct gttacctttac2040  
 agacaggaaa gttccagaaa ctttaagaac aaactctgaa agacctatga gcaaatgg2100  
 ctgaaatact ttttttcaaa gccacatttc attgtcttag tcaaaagcag attattaa2160  
 gattattcaa aattcgtttt tttaaaattg caactccaag atatacaact ttgaaactgg2220  
 aataaggttt tattttctat taataaaaaa gaattgtgac aaaaaaaaaa aaaggcttcg2280  
 gcttttgaa gcttatgtgt ggggggggggt 2310

00673400.122700

## (2) INFORMATION ON SEQ ID NO. 3:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 854 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ctgcacgggg gctcggggtc actataaaag gtgggagcgc gtgggtgccc agcaacgacg 60  
 agtttcagaa cgatggagag ctcccgcggtg aggtctgctgc cctccctggg cgcgcgcttg120  
 ctgctgatgc tacctctgtt gggtaacctg gccacgagg agcgcgagct ccagccccga180  
 gccctggaca tctactctgc cgtggatgat gccctccacg aqaaggagct gatcgaaagcg240  
 ctgcaagaaq tcttgaaqaa gctcaagagt aaacgtgttc ccatctatga gaagaagtat300

ggccaagtcc ccatgtgtga cgccggtgag cagtgtgcag tgaggaaagg ggcaaggatc360  
 gggaaagctgt gtgactgtcc ccgaggaaacc tcttgcaatt ccttcctcct gaagtgtta420  
 tgaaggggcg tccattctcc tccatcacac cccatccctc tactttcccc agaggaccac480  
 accttctccc ctggagtltt gcttaagcaa cagataaagt ttttatcttc ctctgaagggg540  
 aaagggtctt tttcctgctg tttcaaaaat aaaagaaacac attagatgtt actgtgtgaa600  
 gaataatgcc ttgtatggtg ttgatacgtg tgtgaagtat tcttatctta tttgtctgac660  
 aaactcttgt gtacctttgt gtaaaagaag gaagctttgt ttgaaaattg tatcttttga720  
 tgtggcatgg cagaatgaaa attagatcta gctaattctg gtatgtgtca ttacaacctg780  
 gaaaaataat caccctaaat gacacaaatt gaagcatgta caaattatca ataataaagt840  
 gtttttaata attg 854

## (2) INFORMATION ON SEQ ID NO. 4:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1112 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```

cgccagcccc gtcggggggcc cggagggggac tcggagcggg ccaagggggg gctccggggg 60
gcggaactcgg agcggggggcc ggagtgaccg ggacagctgt cctctctgac accaccccgg 120
cctgcctctt tgttgccatg agagctgcct acctcttctt gctattcctg cctgcaggct 180
tgctgggtca gggccagtat gacctggacc cgctgcccgc gttccctgac caggtccagt 240
acaccccacta tagcgcaccag atcgacaacc cagactacta tgattatcaa gaggtgactc 300
ctcggccctc cgaggaacag ttccagttcc agtcccagca gcaagtccaa caggaagtca 360
tcccagcccc aaccccagaa ccaggaaatg cagagctgga gccacacagag cctggggctc 420
ttgactgccc tgaggaacag tacccgtgca cccgcctcta ctccatacac aggccttgca 480
aacagtgtct caacgaggtc tgcttctaca gcttccggcg tgtgtacgtc attaacaaag 540
agatctgtgt tcgtacagtg tgcctccatg aggagctctc ccgagctgac ctctgtcggg 600
accaagtctc caaatgtggc gtgatggcca gcagcggcct gtgccaatcc gtggcggcct 660
cctgtgccag gagtgtggg agctgctagg gtggtgctgg catcctgagt cctggccctc 720
ctgggactcg gggccctcgg gccctgcctg acctggtgct tttttcccca tcccattgtt 780
ccttttattc tgtaaaaagt tagtggactg cagccctggg ggttgcaaggc tgcggtgctc 840
caggccccc cttcagcccg tggccacctc tgggggcacga tggggggctcc ccaactgccc 900
gtctgcccct cgggttgggg gagtatcccc ggctctctg tgggacccctg ggccttgacg 960
ggccttctca gccccgtttt aggacagaca gtcccccgag gtaggctaca tccccccacc 1020
ccagctgggtc tgcctggatt tctacagcc cccgtgggca tggaccacct ttattttatal 1080
caaaattaaa aacaagtttt tacaacaaaa aa 1112

```

(2) INFORMATION ON SEQ ID NO. 5:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1051 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:

002221-004E960

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

```

gcgcaggcgc gaagaagctg gcagggggcac gagccggggg cgggtttgaa gacgcgtcgt 60
tgggtttttg aggcocgtgaa acagcccgttt gagtltggct gcgggtggag aacgtttgtc 120
aggggcccgg ccaagaaggaa ggcocccctg ttacgatggt gtccatgagt ttcaagcgga 180
acgcagctga cgggtttctac agcacccggg gctgcggctg ttgccatgtc cgcacccggga 240
cgaatcatct ggggacctgg tacatggtag taaacctatt gatggcaatt ctgctgactg 300
tggaaagtgc tcatccaaac tccatggccag ctgtcaacat ccagatgtaa gtcatcggtg 360
attactattc gtctgagaga atggctgata atgctgtgtt tctttttggc gtctctgttc 420
ttatgtttat aatcagttca atgctgggtt atggagcaat ttcttatcaa gtgggttggc 480
tgattccatt ctctctgttac cgactttttg aactctgtct cagttgcctg gttgctatta 540
gtctctcac ctatttgcca agaatacaag aatatctgga tcaactacct gattttccct 600
acaaagatga cctcctggcc ttggactcca gctgcctcct gttcattggt ctgtgttct 660
ttgccttatt catcattttt aaggcttacc taattaaactg tgtttggaac tgcataaaat 720
acatcaacaa ccgaaacctg ccggagattg ctgtgtacct tgcctttgaa gcacctccct 780
agtacgtttt gccaacctat gaaatggccc tgaataatgcc tgaataaaga ccaccacctc 840
cttacttacc tgcctgaaga aattctgccc ttgacaataa atccataacc agctttttgt 900
ttgtttatgt tacagaatgc tgcaattcag ggtctttcaa acctgtttag atataaaata 960
tgggtggccct ttggttttaa agcaatttat ttcccaaaac actaagggag cctttttgga 1020
catctcggtta aacggccctt ttgggttttt t

```

(2) INFORMATION ON SEQ ID NO. 6:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1516 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

00673400.12200

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

```

gttgctctca tccctctcat acaggggtgac caggacgttc ttgagccagt cccgcacgag 60
caggggggaag aagatcccatg agaaggagaa gcgcctggag gcaggagacc accccgtgga 120
gctcgctggcc cgggacttcg agaagaacta taacatgtac atcttccctg tacactggca 180
gttcggccag ctggaccagc accccattga cgggtacctc tcccacaccg agctggctcc 240
actgcgtgct cccctcatcc ccatggagca ttgaccacc cgttttttcg agacctgtga 300
cctggacaat gacaagtaca tcgccttggg ttggtgggct ggctgcttcg gcattcaagca 360
gaaggataac gacaaagatc ttgtgatcta aatccactcc ttccacagta cgggattctc 420
tcrttaaccc tccccttcgt gtttcccca atggttaaaa tgtttggatg gttgttgtt 480
ctgcctggag acaaggtgct aacatagatt taagtgaata cattaacggt gctaaaaatg 540
aaaattctaa cccaagaaca tgacattctt agctgtaact taactattaa ggcctttttc 600
acacgcatta atagtcctat tttctctctg ccatttggag ctttgcccat tgccttatgg 660
ggcacatggg gtggaccagg atctgtctgg ctctgctcta aacacacatt gcaagcttcaa 720
cttttctctt tagtgttctg ttgaaaacta atacttaccg agtcagactt tgtgttcatt 780
tcatttcagg gtcttggctg cctgtgggct tccccagggt gcttgagggt gggcaaaagg 840
aagtaacaga cacacgatgt tgtcaaggat ggttttggga ctagaggctc agtgggtggg 900
gagatccctg cagaacccac caaccagaac gtggtttgct tgaggctgta actgagagaa 960
agatcttggg gctgtgttat gaaaataatg acattctcac ataaagccag ttcatcacca 1020
tttctctctt tacctttcag tgcagtctct tttcacatta ggctgttggg tcaaaccttt 1080
gggagacagg actgtcagtt cctcgggaag tggtcagcgc atcctgcagg gctctcctct 1140
ctctgtcttt tggagaacca gggctctctc caggggctct agggactgcc aggcctgttc 1200
agccagggaag gccaaaatca agagttagat gtagaaagt gtataataga aaaagtgga 1260
gtgtgaaatc ggttgtctct tcttcacatt tggatgatgt tcataagggt tttagactgt 1320
tctctctttt cttccacctc cctctttttt ccccaagaa acagagaaaa ctcaaggtta 1380
atggggaggg tcggatccta caggcctgag aatcgggtcaa cttcaagcat ttcatggaaa 1440
aggcgggttc ctaatttaac ctacaaaccc ccacccagga tggtagaggg tttccacaa 1500
tcctccaaaa ataaaaa

```

## (2) INFORMATION ON SEQ ID NO. 7:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2367 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

09673400.12200

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

```

cgccggggact cttggcggggt gaagggtgtgt gtcagctttt ggcgcactcg agccctgggc 60
gcgccttgctt aaagagccga gcacgcgggt ctgtcatcat gtccgcgttac gggcgggtacg 120
gaggagaaac caaggtgtat gttggtaacc tgggaactgg cgcctggcaaa ggaaggttag 180
aaagggtcttt cagttattat ggtcccttaa gaactgtatg gattgcgaga aatccctcag 240
gattcgcctt tctggaatcc gaagatcccta gagatgcaga agatgcagta cgaggactcg 300
atggaaaggtt gatcttgggc tcccgagtga ggggtgaact atcgacaggc atgcctcgga 360
gatcaacgttt tgatagacca cctgccccgac gtccctttga tccaaatgat agatgctatg 420
agctggggcga aaaggacat tatgcttatg attgtcatcg ttacagccgg cgaagaagaa 480
gcagggtcacg gttcatagta cattctctgat ccagaggaa ggcgtactct cgtctcacga 540
gcaggagcag gggacgaagg tcaagggtcag catctctctg acgatcaaga tctatctctc 600
ttctgtagatc aaagatcagct tcaactcagaa gatctagggtc tgggtctata aaaggatcga 660
ggtatttccca atccccgtcg aggtcaagat caagatccag gtctatttca cgaccagaaa 720
gcagccgcatc aaagtccaga tctccatctc caaaaagaa tcgttcccca tccaggaaatc 780
ctcgcagaag tgcaagctct gaaagaatgg actgaaagct tcaagttcac cctttaggga 840
aaagtatttt tgtttacatt attataaagg atttctgatg tctgtaaaat gtaacctagg 900
aaagataaatt caaccatcta atcaaaaagg atctggatta ctatgtaaa tccacgacgt 960
aagataaatat aaattttggt gaatgtatta acatcatatg gtctgaaaat tggggttttt 1020
atttggccaca tttaaaataa atgttttcta ctagattttt gatttgtgtt caatattaac 1080
acttcttaatt tggatatatt tgagagtcag acattataat tgttaacctt attcatatat 1140
acctacattc agaattgaaa ggtgttgggt aaagtcttga catcactatt ctatgcataa 1200
aacttggcca ggtactttaa ggaactttgaa aattccatct tacctttgta gctctgggtal 1260
agatgacctg agtcccttat gatacagcct gaatgcata tgacagatcc ttaagtttag 1320
taattccgtt gaagtgtgtg tttagtagta ttgtatgac agtggtgtag caagtgcag 1380
caactgattg tctaaatgag catgcacgga actaaacgaa actgattaaa tgtatgagaa 1440
atagaaaatg atttctggat gatctttata ctaattcgag ctttcaggct actagttggc 1500
atagtgtttaa ttaggactcc ccaagatag gggagtctta ctctcaatgg tcttgtttct 1560
ttgctttcta cattagttaa ccagttttat accaaaaaaa gcatgtttga ggaactgtct 1620
gaaattggga caaaaacact tcatgtaaac cagcttttga aaattttcca gccagatac 1680
tcttctatcta tccaatgga ttgtcttatt ctgagcaaa acctgttgtt aatcttcaa 1740
ctagggtttg cagttcccaa ccacaacatt ctctattttt gccaggctgg tgcaaatgaa 1800
ttaaagatgt caatcagaaa tgtcaatgag actaaagtgg ttttgtaaat ctacgtcata 1860
tttagcagca tcccatgtag ctaatatttt ttggtagcat ctggtagacc ttagaatgtt 1920
acatagccag taggttcttt attcaaat tttaagtatctt aagaatagta gggcagtaac 1980
agttactttt gagagttttt tggccaagct ttaccaggc attctctcag ctctgttaca 2040
aaaaaaataa aacctgctgg ttgcgcagat acctaggctt tctcaatttt tgcattctag 2100
caaaagtcat ggaatactatt gcaacttggg aataactggc tgcatcaagt ttattcgtat 2160
gtttgaccgc tagtatgttg gaagtatttt ggatttgttt tgggaatttt actggctgaa 2220
ttatgttttg tataaagtta tgtgtataac tggcaggctt acttatctgt tgcacttgtt 2280
tagctttaat tgttctgtat tattttaaaga taagtcttact caacaataaa tctgcagaga 2340
tggaacaaat aaaaaaaaa aaaaaaa

```

2367

09673400.122700

## (2) INFORMATION ON SEQ ID NO. 8:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 568 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

ctcgagccgt gggcagtgcc gcggaatgcg cggagacact gaccttcagc gctctgggtc 60  
 cagcgccatg ggcgcctcca ggaagtcttt cgttggggga aactggaaga tgaacggggcgl20  
 gaagcagagt ctggggggagc tcatcggcac tctgaacgcg gccaaaggtgc cgcccgacac180  
 cgaggtggtt tgtgctcccc ctactgccta tatcgacttc gcccggcaga agctagatcc240  
 caagattgct gtggctcgcc agaactgcta caaagtgact aatggggcctt ttactgggga300  
 gatcagccct ggcgatgatca aagactgcgg agccacgtgg gtggtcctgg ggcactcaga360  
 gagaaggcat gtctttgggg agtcagatga gctgattggg cagaagaagg cccatgctct420  
 ggcaagggga ctcggaagtaa tcgcctgcac tggggagaag ctagatgaaa ggggaagctgg480  
 catcactgag aatgttgttt tcgagcagac aaagggcacc ggggatgact tgaaggactg540  
 gatcaagttc gtcttgccct gtcggcct 568

## (2) INFORMATION ON SEQ ID NO. 9:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1775 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN

## (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

ctccgggggcc atttttgtgaa gagacgaaga ctgagcgggtt gtggccgcgt tcgccacccc 60  
 cagcagcagct cgggtttctct acgcagaacc cgggagtagg agacttcagaa tcgaatctct 120  
 tcctccctccc cctcttgcga gatttttttg atcttcagct acatttttcgg cttttgtgaga 180  
 aacctttacca tcaaacacga tggccagcaa cgttaccaac aagacagatc ctgcgtccat 240  
 gaactcccggt gttattcattg ggaattctcaa cactcttctgt gtcaagaagt ctgatgtgga 300  
 ggcaatcttt tcgaagtatg gcaaaattgt gggctgctct gttoataagg gctttgcctt 360  
 cgttcagtat gttaatgaga gaaatgcccc ggctgctgta gcaggagagg atggcagaat 420  
 gattgtctggc caggttttag atattaacct ggctgcagag ccaaaagtga accgaggaaa 480  
 agcaggtgtg aaacgatctg cagcggagat gtacggctct tcttttgact tggactatga 540  
 ctttcaaccgg gactattatg ataggatgta cagttaccca gcacgtgtac ctctctctcc 600  
 tcctattgct cgggctgtga tgccctcgaa acgtcagcgt gtatcaggaa acacttcacg 660  
 aagggggcaaa agtggcttca attctaaagag tggacagcgg ggatcttcca agtctggaaa 720  
 gttgaaaagg gatgaccttc aggccattaa gaaggagctg acccagataa aacaaaaagt 780  
 ggaattctctc ctggaaaaacc tggaaaaaat tgaaaaaggaa cagagcgaac aagcagtaga 840  
 gatgaagaa: gataagtcag aagaggagca gacgacgagc tccgtgaaga aagatgagac 900  
 taatgtgaag acggagctcg aggggggtgc agatgactct gctgaggagg gggacctact 960  
 ggatgatgat gataatgaa atcggggggga tgaccagctg gagtgtgatc aggatgatga 1020  
 aaaaagggct gagggaaggag aggatgacag agacagcgcc aatggcgagg atgactctta 1080  
 agcacatagt ggggtttaga aatcttatcc cattatttct ttacctaggc gcttgtctaa 1140  
 gatcaaattt ttcaccagat cctctccccc agtatcttca gcacatgctc actgttctcc 1200  
 ccattcttgt ccttcccatt ttcatttaatt catattgccc cgcgcctagt cccattttca 1260  
 ctctctttga cgcctccagt agttttgtta agtcttaccg tgtaattttt gcttttaatt 1320  
 ttgatcacctc tttatgactt aacaataaaa aggatgtatg gtttttatca actgtctcca 1380  
 aaataatctc ttgttatgca gggagtacag ttcttttcat tcatacataa gttcagtagt 1440  
 tgctctcccta actgcgaaagg caatctcatt tagttgagta gctcttgaaa gcagcctttga 1500  
 gttagaagta tgtgtgttac accctcacat tagtgtgctg tgtggggcag tccacacaaa 1560  
 atgtatacaat gratttttgt gaattgagagt tggcatgtca aatgcacctt ctagaaaaat 1620  
 aattagtggt atagtcttaa gatttgtttt ctaaaagtta tactgtgggt tatttttgtg 1680  
 aacagccctga tgtttgggac cttttttctt caaaaataac aagtccttat taaaccaggal 1740  
 atttggagaa aaaaaaaaaa aaaaaaaaaa aaaaaa 1775

(2) INFORMATION ON SEQ ID NO. 10:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 509 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:



- (A) ORGANISM: HUMAN  
(C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

```

caggctcgagt ggccactgcg cagaccagac ttcgctcgta ctgctgccc tcgcttcgct 60
tttcctccgc aacctgtct gacaaacccg atatggctga gatcgagaaa ttcgataagt120
cgaaactgaa gaagacagag acgcaagaga aaaatccact gccctccaaa gaaacgattg180

aacaggagaa gcaagcaggc gaatcgtaat gaggcgtgcg ccgccaatat gcaactgtaca240
ttccacaagc attgccttct tattttactt cttttagctg ttttaacttg taagatgcaa300
agagggttga tcaagtttaa atgactgtgc tgcccttttc acatcaaaag gactacttga360
acaacggaa ggcgcggcc tacctttccc atctgtctat ctatctggct ggcagggaag420
ggaagagtgc caggttggtg aggaagaaag ggggtggaag aagttggatg ggcgccag480
aaaacttggg taaaccgaac ttggccaag 509

```

(2) INFORMATION ON SEQ ID NO. 11:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2191 base pairs  
(B) TYPE: Nucleic acid  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN  
(C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

002221 004260

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

```

actgagcgaagg ggcagccgct ggcggcatcta caccgagcgc tgtggctccg gccctcgctg 60
ccagccgctcg cccgacgagg cgcgacccgt gcagcgccgc ctggacggcc gccgggctctg 120
cgtcaaacgct agtgcgcgtca gcgcgctgcg cgcctacactg ctgccagcgc cgcgcgctcc 180
aggaaatgct agtgagtcgg aggaagaccg cagcgccggc agtggtggaga gcccgctccg 240
ctccagcagc caccgggtgt ctgatcccaa gttccacccc ctccattcaa agataatcat 300
catcaagaaa gggcatgcta aagacagcca gcgtcaaaa gttgactacg agtctcagag 360
cacagatacc cagaacttct cctccgagtc caagcgggag acagaaatcat gtccctgcgc 420
tagagaaatg gaagacacac tgaatcacct gaagtctctc aatgtgctga gtcccgaggg 480
tgtacacatc cccaactgtg acaagaaggg attttataag aaaaagcagt gtccctcttc 540
caaaaggcagg aagcggggct tctgctggtg tgtggataag tatgggcagc ctctcccagg 600
ctacaccacc aagggggaag aggaagtgca ctgctacagc atgcagagca agtagacgcc 660
tgccgcgaag ttaatgtgga gctcaaatat gccttatttt gcacaaaaa ctgccaaagg 720
catgaccagc agctggctac agcctcgatc tatattttct tttgtgtg actgattttt 780
tttaaaccaa agtttagaaa gaggtttttg aaatgcctat ggtttctctg aatggtaaac 840
ttgagcatct ttctactttc cagtgtcag caaagagcag ttgaaattt ctgtctgctt 900
cctatcaaaa tattcagaga ctgcagcaca gcacccagac ttcatgccc cgtggaatgc 960
tcaccaatg ttggctgaag cggccgacca ctgactttgt gacttagggc gctgtgttgc 1020
ctatgtagag aacacgcttc acccccactc ccgctacagt gcgcacaggg tttatcgaga 1080
ataggaaaac cttttaaacc cggctatccg gacatcccaa cgcctgctcc tggagctcac 1140
agcctctctg ggtgcattct ctgaaaccaa ggctgtgact cctcaaccaa gaagaatgtt 1200
tatgtcttca agtgacctg actgcttggg gactattgga gaaaaaagg tggagtctat 1260
cttgtttcaa aaatatgtat ctaagaatgt tctagggcac tctgggaacc tataaaggca 1320
ggtattctcg gccctcctct tcaggaaatc tcttgaagac atggcccagt cgaaggccca 1380
ggatggcttt tgcctgggta ccgtggggtg gaggggagag agagcaggg agagctcagg 1440
tcacatctca gaggcacac aagtaatggc acaattcttc ggatgactgc agaaaaatag 1500
gttttgtgat tcaacaaact aagacgaagc ttattttctg ggataagctc tttaaaaggca 1560

aagcttttatt ttcatctctc atcttttctc ctcccttagca caatgtaaaa aagaatagta 1620
atatcagaagc aggaaggagg aargccttgc tggggagccc atccaggaca ctgggagcac 1680
atagagattc acccatgttt gttgaactta gactcatctc catgcttttc ttataaattc 1740
acacatatat gcagagaaga tatgttcttg ttaacatgtg atacaacata gccccaaata 1800
tagtaagatc tatactagat aatcctagat gaaatgttgc agatgctata tgatacaact 1860
tagggcatga ctgaggaagg gagctcacgc ccagagactg ggtgctcttc ccggaggcca 1920
aacccaaaga ggtctggcaa agtcaggctc aggggagact tgcctctgct cagacctcgg 1980
tgtggacaca cgctgcatag agctctcctt gaaaaacaga ggggtctcaa acattctgcg 2040
tacctattag cttttcttta tttttttaac tttttggggg gaaaagtatt tttjagaagt 2100
tctcttgca atgtatttat aaatagtaaa caaagttttt accattaaaa aaaaaggagg 2160
taaaaagaaa aaaaaggagg gccgcccact a
2191

```

03673400.122700

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 1769 base pairs  
(B) TYPE: Nucleic acid  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:  
(A) ORGANISM: HUMAN  
(C) ORGAN:

(vii) OTHER ORIGIN:  
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

attattttaca	tttcaaaaata	attcccccta	atcggtttac	tcctaagttc	attaccattg	60
ttggcccacc	ttatggttca	ccactrtggt	cttatccccg	ccctgggttc	aaacagggac	120
attggcaaac	gacacagaca	agaggggttc	cgtagtcgca	ctctcccaac	cgcaattcat	180
ttatgtagac	gcacaggggc	agctcccgca	cggtctttct	aggctcctgc	cgggagcctcg	240
agggctagac	agcggggaag	caggcagatg	tcggggagat	gcagcaggac	ctcaccagga	300
ggcggaacgg	ccacggggag	ggggcccccg	gacattctgc	agcaaggagg	ctgcaggggc	360
tcggccctgc	ggcgcccgct	ccacgaggca	ctgcggccca	gggtctggtg	cggaaggggc	420
ggccagtggc	cttgtgtgac	ctgtattgcc	tcacgcctgc	gccctccgtg	ctggctttggc	480
agacagtaca	gcatccaggg	gagtcacaagg	gattggggcg	gaccagactg	ggcgagggcg	540
ggcgggcgga	gtgaaatgac	cttcaggagag	cgatgtggtg	caggcagggt	tgaggagcgc	600
agggggccgc	gagcggggag	cactggcctc	cagatccctg	ggcccaaggc	ggctctccgc	660
ggcgggcagc	agccggggtc	ggtgtccctag	cttctgggtg	ggagcagggc	ccaggtcttc	720
agctgggggt	gagctgtcca	ccagctgcgc	aaaggcaaac	gccaggtccg	gtggacgtga	780
caagcaggac	attgacatgt	ccgggtgtgac	ggcgaggaca	gaggaggggc	gtccggcctct	840
ctcgaaacac	ttatgctgtg	cggtgcgcgc	caagaagctc	ctctgtttct	ttactcttc	900
cgcgagttgc	gcacacatct	gctgcctctt	ggatcccgac	aaccccaaac	atgaagaaga	960
ttgtgctact	caagctcaag	cttgcggctt	gaaatccggc	acaaaacctc	ctagcttggal	1020
aatgacatat	ctgcacctta	caaacactgc	actacactgc	tcaggaaatc	ggatcggaag	1080
gtgaaatcgt	aggaacacga	ccctcatcag	cccaactcaa	agacacacat	gcttcagcag	1140
ctcccggaic	acccaccccg	ccacggcgac	tcacattcca	tgggcacccc	ctcggcgggal	1200
cggttgtagca	ccagcgcaca	catcatccca	gagctgagct	cctccacggc	gatgacgcgc	1260
ttcccacatc	ctccctcttc	ttctttttca	tcctcttgct	tttttttctt	tgagctttcc	1320
tgctcttctt	tttttttgag	agattcaaaq	ctctccagct	tttgtttccc	cgctccctttc	1380
tgaatttaat	ttgcactatg	tcattttgac	tggtttgagt	tggtgagagc	gctctgactc	1440
tcagttacac	gtgtcgtgag	tgtgagccac	cttggcaagt	gctctgtcag	ggccccggcc	1500
ccctccatct	gggcgggggt	actggggccc	gggtctgtgc	ccgaggcctc	acctctgccc	1560
ccctagtgtt	ggaaagctcc	accagcatca	cgggagacgc	ttcaagactt	ccattacgccl	1620
ccatctcgct	ctgtgtccct	cccccacagg	gcttcaagca	gagcctcrra	ctcatcatcal	1680
ataaacctct	ttcacgcaaa	aaaaaaaata	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	1740
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa				1760

## (2) INFORMATION ON SEQ ID NO. 13:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1026 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

```

aaaagctgtc cgccggggga gccaggggcc agctttgggg ttgtccctgg acctgtcttg 60
gttccagaac ctgacgaccc gccgacggcg acgtctcttt tgactaaaa acagtgtcca 120
gtgtctccag ctaggagctct acgggggacc cctcccgcgc cggccaccatg cccaacttct 180
cttggcaactg gaaaatcatc cgatcggaaa acTtcgagga attgtctaaa gtgtctgggg 240
tgaaatgtgat gctgaggaag attgtctgg ctgcagcgtc caagccagca gtgagatcca 300
aacaggaggg agacactttc tacatcaaaa cctccaccac cgtgcgcacc acagagatta 360
acttcaagggt tggggaggag ttctgaggagc agactgtgga tggggaggccc tgtaagagcc 420
tggtgaaatg ggagagtgag aataaaatgg tctgtgagca gaagctccctg aaggggagagg 480
gccccaagac ctctgtggacc agagaaactga ccaacgatgg ggaactgatc ctgaccatga 540
cgccggatga cgttgtgtgc accagggtct acgtccgaga gtgagtggcc acaggtagaa 600
ccgcggccga agcccaccac tggccatgct caccgccctg ctctactgcc ccctccgtcc 660
caccgccctc ttctagdata cgctctccct taccocagt cttcttgggg gtctactggga 720
tgctctttgc aggtctctgc ttcttttgac ctctctctc ctcccttaca ccaacaaaga 780
ggaatggctg caagagccca gatcacccat tccgggttca ctcccgcctt ccccaagtca 840
gcagtcctag ccccaaaacca gccacagagc ggtctctct aaaggggact tgagggccctg 900
agcaggaaaag actggccctc tagcttctac cctttgtccc tgtagcctat acagtctaga 960
atatttatct tttaatttta ttaaaatgct ttaaaaaaat aaaaaaaaaa aaaaaaaaaa 1026
aaaaaa

```

## (2) INFORMATION ON SEQ ID NO. 14:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 676 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

000214001 102700

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

```

ggccattttg tgaagagacg aagactgagc ggttggtggcc gcgttgccga cctccagcag 60
cagtcgggctt ctctacgcag aaccggggag taggagactc agaatcgaat ctcttctccc120
tcccccttctt gggcagcaag gcgaacccca tccctactca ctggagctca gctttgattt180
ttaacctccc tttcccaacc ttccagaaca cacacattcc attccaaaac tgattttata240
aagacatttt aaacataatg atgcaacttg gttgtgacta cagcaaatgt acagggtgtt300
tttttttaat tgtttccaaa accggggacct ggatttaaga tgtaattttt aaaattttcta360
ttttctattt ttccggcagca gttgggttag aggaggagga gccttttagc ctcccagaaa420
ctgacctctc tacttccctgc tgtattttta agattgattg atgatgttga aagggtcttg480
ctgtctgctg actgaaaact ttatcctttg ggtttttgtg gaactgcgtt tggaaaagaga540
aaagaaatga accttactga cttgacattt tgcacctccc ggttttccga tctgggcaat600
tttaattttg gttttacagt gagagtttt gatctcagca cagaagtaat ccaattttt660
ttaacatttt ccgact 676

```

(2) INFORMATION ON SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1254 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library

00221-00220

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

```

cggctcgcagc agctcgcagcg gctcaaacac ctcatctgac ctggccagct gaccttcaaa 60
ccctgcattt gaaccgacca acattaaagt cagagagtaa acttgaatgg aataacgaca 120
tccagagaagt taatcatttg aattctgtaac actggagaaa aaccgaaaaa tggacggggc 180
atgaagagac taatcatctg gaaaccgatt tcagtgccga tggcatgaca gagctagagc 240
tcggggcccgag ccccgagctg cagcccatc gcaggccacc gaaagaacct ccccgatag 300
gtgggtccctgg aaaggacatt ttggaagatc aactatatct tcctgtgcat tccgatggaa 360
tttcagttca tcagatgttc accatggcca ccgcagaaca ccgaagttaa tccagcctag 420
cggggagaagt gttgaccaag gtggagaaga atcacgaaaa ggagaagtca cagcacctag 480
aaggcagcgc ctctctctca ctctcctctg attagatgaa actgttacct taccctaaac 540
acagttattc tttttaacct ttttatttgt aaactaataa aggtaatcac agccaccaac 600
attccaaagt accctgggta cctttgtgca gtgagaagta gtgagcatgt gagcaaggcg 660
tgtgcacacg gagactcatc gttataaatt actatctgcc aagagtagaa agaaaggctg 720
gggatatttg ggttggcttg gttttgattt ttgtcttgtt tgtttgtttt gtaactaaac 780
agttattatc ttctgaatcc gtagggaact aagtatatac atgttatcca atcaagatgg 840
ctcagaatgg gctttcttga gtgtctaaaa cttgacaccc ctggtaaatc ttctcaacac 900
cttcacatgc ctgcgtaagt aagttttgat tcatttttta ccaactggaat ttttcaatgc 960
cgctcatttc agttagatga ttttgcactt tgagattaaa atgccatgtc tatttgattal020
gtcttatttt ttatttttta caggcttacc agtctcactg ttggctgtca ttgtgacaaal080
gtcaaaataaa cccccaaggc cgcacacacg tatggatcac atattgtttg acattaaagt1140
tttgccagaa aatgttgcct gtgttttacc tcgacttgcg aaatcgatt agcagaaagg1200
catggctaat aatgttggcg gtgaaaaata ataaaaaagt aaacaaaaag aaaa 1254

```

## (2) INFORMATION ON SEQ ID NO. 16:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 537 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

00227.0012700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

```

ggcccgccggcc cccaccctcg acatgcgctt cggcgcgacgc cttagcgctg acccccacgc 60
aaccacagcga aactccgcgg aggcgcgcgg cagcatggac ggtcgggtgc agctgatgaal20
ggccctcctg gccggggccc tccggcccg gcgcgctcgc tggaggaaac cgattccctt180
tcgccagacg tttgacggag ataccgacgc actcccgag ttcacgtgc agacgtgctc240
ctacatgttc gtggacgaga acacgtcttc caacgacgcc ctgaagggtga cgttcctcat300
caaccggcttc acggggccag cctgcagtg ggtgatcccc tacatcagga aggagagccc360
cctgctcaat gattaccggg gctttctggc cgagatgaag cgagctcttg gatggggaga420
ggacgaggac tctatggccg ggagaccctc gggcctgggg gcgggtgctc tgggaagagt480
tcgctgtgccc agtgggccacc gctagggtct ccacaggcgc cctcccccagg gaatgct 537

```

## (2) INFORMATION ON SEQ ID NO. 17:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 823 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

```

tagactgaac agggagggga gtccctgggta gcgcgccggt ctaaaatcggt acctggccga 60
aagttcccat gagtctttgc cagcgtcccc ctccctttgt gaggattggg atatcccgac120
tccttaaggg cctggcgac atagggtgtg accttttcat tcccgtrgtt atggaggggc180
acatctgcca gagcctggag tctgcgaagg ccgggacccc gttccccggc ccacagtggg240
gggtgtgaaa cccgagagaa ctgggttgca aattcgtgaa gaatcagcat catgtttggc300
agctgagtat tggagccagg agcctgccat gaggtttttg gaacagagtg ctgttttaga360
gctggcagca gcatctcagc ccaagagaa gtttatctcc cagaggatgt cagtcaccaag420
gaccagtagc tgccatcagt ttggattctg aaaaactaac gccatcaaca ctgggtgttag480
aaacatgctt gccttatgta tcagaggaca tgctcagcag atccaaagaga tatattttgg540
aactttttct agaaaaggca cattgggtat cattcattac attcttgagg tttttttggg600
tttttttttt ttttttttga gacagtcttg ctgtattgoc caggcttgga gttgtgtggc660
acaatcacag ctcatgtcat cctcaatcac ccagggccta agcaatcttc ccaaccttga720
gctggacta cagctcacag cacaccgggc taataatttt tttgttgag acggtttttc780
tatgttgccc ggggtgtttt cagggtccgg ggttcagatg gtc 823

```

0071400\*12700 0072257 0074290

## (2) INFORMATION ON SEQ ID NO. 18:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1082 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

```

gggcgcacat aaggtgtgac cttttcattc ccgttgttat ggagggccac atctgccaga 60
gcctggagtc tgcgaaggcc gggaccocgt tcccgggcc acagtggggg tgtgcaaac 120
cgagagaact ggtcgctgaa acctctacaa cttagtgtgac cgttaactgcc agagccctgc 180
cctgaattcc tgcctttact cctcttttaa gattgcgtac ccactgcaga gtgctgaaga 240
cggggtagcc acgaggttgc aaattcgtga agaatacagca tcatgttttg cagctgagta 300
ttggagccag gaggcctgcc tgaggttttg agaacagagt gctgttttag agctggcgag 360
agcatctcag cccaagagaa ggtatatatt ccagaggatg tcagtcacca ggaccagtag 420
ctgccatcag tttagattct gaaaactaac tggcatcaac actgggttga gaacatgct 480
tgcccttatg atcagaggac atgctcagca gatccaagag atatatattg caactttttc 540
tagaaaaggc acattgggta tcattcatta cattcttgag tttttttggg tttttttttt 600
ttttttttga gacagtcttg ctgtattgcc caggctggag tgtggtggca caatccacag 660
tcattgcctc ctcaatcacc caggcctaaq caatcctccc accttgtagc tgggactaca 720
gctcacagca cacctggcta aaattttttt tttgttgaga cggattctct atgttgccca 780
ggcgtgtctc aggtcctctg gctcagatgg tccctcctgc tcagcttcca aaggcacagg 840
cgaagtctta gctttgtccc ttgccatcat gcccaacaag aggttctata ccttttaagt 900
aattgacttt cataaatcgg ttatgttggt gggcaagttc ttttaagctgg aaattgtaaa 960
ttcctcctga aatgtttttt catgcagtta ccatgaacta atactacaaat aaaggatggt 1020
cttgggtgtc aaaaaaaaaa aaaaaaaaaa aaaaagaaaa aaaaaaaaaa aaaaaaaaaa 1080
aa                                                    1082

```

## (2) INFORMATION ON SEQ ID NO. 19:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1548 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

09573400.122700



- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

cccattccat aggggaatgag ctggggtgtc cttttctccc acgttcaccc gcacttcgtt 60  
 agagagcagt gtccacatgc cacaccacaa gatccccaca atgacataac tccattcaga 120  
 gactggcggtg actgggctgg gtctcccccac ccccccttc agctcttga tcaactcagaa 180  
 tctggcagcc agttccgtcc tgacagaagt cacagcatat attggtggat tcttgtccat 240  
 agtgcactctg ctttaagaat taacgaaaagc agtgccaaga cagttaaggat tcaaacccatt 300  
 tgcacaaaat gagtctaagt gcattttactc tcttccctggc attgatcgtt ggtaccagtg 360  
 gccagactta tgattatgat tttccctat caatttatgg gcaatcatca ccaaacctgtg 420  
 caccagaaatg taactgcccc gaagctcacc caagtgccat gtaactgtgt gagctgaaac 480  
 tgaaaaagtgt accaatgggtg cctctctggaa tcaagtatct ttaccttagg aataaccaga 540  
 ttgacctat tgatgaaaaa gcttttgaga atgtaactga tctgcagtg ctcattctag 600  
 atcacaaacct tctagaaaaa tccaaagataa aaggggagagt tttctctaaa ttgaaacaaac 660  
 tgaagaagct gcataataac cacacaacacc tgacagagtc tctggggccca cttcccaaaa 720  
 cctctggagga tctgcagctt actcataaca agatcacaaa gctgggctct tttgaaggat 780  
 ttgtaaacct gaccttcacat catctccagc acaactcggct gaaagaggat gctgtttcag 840  
 ctgcttttaa aggtctttaa tcaactcgaat accttgactt gagcttcaat cagatagcca 900  
 gactgccttc tgggtctccct gtctctcttc taaactctta cttagacaac aataagatca 960  
 gcaacatccc tgatgagtat ttcaagcgtt ttaatgcatt gcagtatctg cgtttatctc 1020  
 acaacgaact ggctgatagt ggaatacctg gaaattcttt caatgtgtca tccctggttg 1080  
 agctggatct gtccctataac aagcttataa acataccaac tgtcaactga aaaccttgaa 1140  
 acctattact ggaggtcaat caacttgaga agtttgacat aaagagcttc tgcagatccc 1200  
 tggggccatt atccctactcc aagatcaagc atttgcgttt ggaatggcaat cggatctcag 1260  
 aaaccagctt tccaccggat atgtatgaat gtctacgtgt tgctaacgaa gtcaactctt 1320  
 attaatatct gtatcctgga acaatatctt atggttatgt tttctgtgt gcagttttc 1380  
 atcagtatcca tatcttatta ctgtttatta ctcccatgaa tttttaaatt tgagggaatt 1440  
 gttttgtaaa catttatttt tttttaaagg aaaaggatgg aaaggccagg gcctaatttc 1500  
 catccaccaa ggaacacacc acattattcc acggaatagg ccaatcggg 1548

(2) INFORMATION ON SEQ ID NO. 20:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 844 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

007340.122700

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

acctgcagag gggtccatac ggcgttcttc tggattcccg tcgtaactta aagggaatt 60  
 ttcacaaagt ccggagccct tgaatgacct caaatgaagg agggaggatg ccttaagtcc120  
 cttgcagcag gaacccactt aggtggccacc aatcttgact tccagatgga acagtacatc180  
 tataaaagg aasgtgatgg catctatata ataaaatctca agagggaacct ggagaagctt240  
 ctgctggcag ctgctgcaat tgttgccatt gaaaaccctg ctgatgctag tgttatatcc300  
 tccagggaata ctggccagag ggcctgtgctg aagtittgctg ctgccactgg agccactcca360  
 attgctggcc gcttcaactcc tggaaaccttc actaaccaga tccaggcagc cttccgggag420  
 ccacggcttc ttgtggttac tgaacccagg gctgaccacc agcctctcac ggaggcatct480  
 tatgttaacc tacctaccaa tgcgctgtgt aacacagatt ctccctctgc ctatgtggac540  
 attgcaatcc catgcaacaa caaggtaatg attttaggat ctagagtctg tgaatgcgtg600  
 ctctagaaaa aacattcctg tgcacattgt tagagcttgg agttgaggct actgactggc660  
 cgatgaactc gcaagtgtag gtatgtgtgt acatgagggg caagtcttcg ctaacaccac720  
 aagggtctct ggcccaatga gtggagtctg atagttaatt ttgctacaaq tataaccatta780  
 ctgcatgaca gctttgtgga gaaatgaaaa catttggaaa atagtgtgtt ctctgcctct840  
 tcca 844

(2) INFORMATION ON SEQ ID NO. 21:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 862 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library

00221.0042950

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

```

gagcaagaga gaaggaggcc cagacagtga gggcaggagg gagagaagag acgcagaagg 60
agagcgagcg agagagaaaag ggttctggat tgggggggag agcaaggagg ggaggaaggc120
ggtagagagag cggggggccc cgggagggtg aaagggggga ggagaagggg ggggcacgga180
ggcccgagcg agggacaaga ctccgactcc agctctgact tttttcggg ctctcggct240
ccactgcagc catgtcaact ctcttgctgg tggctctcagc ccttcacatc ctgattctta300
tactgctttt cgtggccact ttggacaagt cctggtggac tctccctggg aaagagtccc360
tgaatctctg gtacgactgc acgtggaaca acgacaccaa aacatggggc tgcagtaatg420
tcagcgagaa ttggtggctg aaggcggtgc aggtctctat ggtgctctcc ctcatctctt480
gtgtgtcttc ctctcatctg ttcatgttcc agctctacac catgcgacga ggaggtctct540
tctatgccac cggtctctgc cagctttgca ccagcgtggc ggtgtttact ggcgcttga600

tctatgccat tcacgcccga gagatcctgg agaaagcacc ccgagggggg agcttcggat660
actgcttcgc cctggcctgg gtggccttcc cctcggccct ggtcagcggc atcatctaca720
tccacttacg gaagcgggag tgaagcgcgc cctcgcctcg gctgcgcccg ccccttcccc780
gcccccttcg ccgcgcgttc tccaaaaaat aaaaccttaa ccgcggggaa aaaaaaaaaa840
aaaaaggaa gaaaaaaaaa aa                                     862

```

## (2) INFORMATION ON SEQ ID NO. 22:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 546 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

```

cccagcgaag ggtccttcag gtaggaggtc ctgggtgact ttggaagtcc gtagtgtctc 60
attcgagata atttttagct tagggcctgg ttggttagtc ggttctctcc ttccagtcg120
gagactctcg ccgcaaacat gctccgcca acatctggtc aggccaaaga gcatccgagc180
ttgatccccc tctttgtatt tattggaact ggagctactg gagcaacact gtatctcttg240
cgctcggcat gtttcaatcc agatgtttgt tgggacagaa ataacccaga gcccttggaa300
aaactgggtc ccaatgatca atacaagtgc tactcagtga atgtggatta cagcaagctg360
aagaaggaaac gtccagatct cttaaatgaaa tgtttcacta taacgctgct ttgaaatgaa420
ggtctctccag aagccacatc cgacacaatt tccacttaac caggaaatat ttctcctctt480
aaatgaatga aatcaatggt ggggggcgct attggaagcc ctattggggg tcaagtgttg540
aataaa

```

546

00221.004E756

## (2) INFORMATION ON SEQ ID NO. 23:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1591 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

ggcgaggagc cgagcccgcc acccccccgc cgcgccgcgc cgcgccatggg ctgcctcggg 60  
 aacagtaaga ccgaggacca gcgcaacgag gagaaggcgc aggtgaggcc aacaaaaaga 120  
 tcgagaagca gctgcagaag gacaagcagg tctaccgggc caggcaccgc ctgctgctgc 180  
 tgggcgctgg agaattctgt aaaaagcacc ttgtgaagca gatgaggatc ctgcatgtta 240  
 atgggtttta tggagacagt gagaaggcaa ccaaaagtga ggacatcaaa aacaacctga 300  
 aagaggcgat tgaaccatt gtggccgcga tgagcaacct ggtgcccccc gtggagctgg 360  
 ccaacccccg gaaccagttc agagtggact acattctgag tgtgatgaac gtgcctgact 420  
 ttgacttccc tcccgaattc tatgagcatg ccaaggctct gtgggaggat gaaggagtgc 480  
 gtgcctgcta cgaacgctcc aacgagtacc agctgattga ctgtgccag tacttccctg 540  
 acaagatcga cgtgatcaag caggctgact atgtgccag cgatcaggac ctgcttcctg 600  
 gccgtgtcct gacttcttga atctttgaga ccaagttcca gttggacaaa ctcaaacttc 660  
 actggtttga cgtgggtggc cagcgcgatg aacgccgcaa gtggatccag tgcctcaacg 720  
 atgtgactgc catcatcttc gtgggtggca gcagcagcta caacatgttc atccgggagg 780  
 acaaccagac caaccgcctg caggaggctc tgaacctctt caagagcatc tggaaacaaca 840  
 gatggctgag caccatctct gtgatctctg tcttcaacaa gcaagatctg ctgcctgaga 900  
 aagtcctctg cgggaaatcg aagattgagg actactttcc agaatttctg ctgcacacta 960  
 ctcttgagga tgcctactcc cagcccgagg aggaaccacg cgtgaccctg gccaaagtact 1020  
 tcatttcgaga tgagtttctg aggatcagca ctgccaagtgg agatggggct cactactgct 1080  
 accctcattt caccctgcgt gtggacactg agaacatccg ccgtgtgttc aacgactgcc 1140  
 gtgacatcat tcagcgcatg caccctctgt agtacagct gctctaagaa gggaaaccccc 1200  
 aaatttaatt aaagccttaa gcacaattaa ttaaaagtga aacgttaattg tacaagcagt 1260  
 taactcaacca ccatagggca tgattaacaa agcaaccttt cccctccccc gagtgtattt 1320  
 gcgaaacccc cttttccctt cagcttgctt agatgttcca aatttagaaa gcttaaggcg 1380  
 ccttcagaaa aaaggaaaaa aggcacaaaa agttcccttc caacttcagt aaaaaataat 1440  
 aaaaacagcag cagcaaacaa ataaaaagaa ataaaagaaa caaatgaaat aaattattg 1500  
 ttgtgcagca ttaaaaaaaa tcaaaataaa aatttaaatg gagcaaaagg aaaaaaaaaa 1560  
 ggcaaaaggg gaaagaagaa aaggggggggg g 1591

002221.0042660

## (2) INFORMATION ON SEQ ID NO. 24:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 441 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

```

ggcaggcaga tacgttcgtc agcttgctcc tttctgcccg tggacgcgcg cgaagaagca 60
tcgttaaagt ctcctttcac cctgccgtca tgcctaaagtc agagtctcct aaagagcccg120
aacagctgag gaagctcttc attggagggg tgagctttga aacaactgat gagagcctga180
ggagccattt cgagcaatgg ggaacgcctca cggacttgtt ggtaatgaga gatccaaaca240
ccaagcgctc caggggcttt gggtttgcca catatgccac tgtggaggag gtggatgcag300
ctatgaatgc aaggccacac aaggtggatg gaagagtgtt ggaaccaaag agagctgttt360
cagagaagat ttgaaaagcc aggtgccact tacctgtgaa aaggtatttg ttggtggatt420
aaggagcact tgagacatca c

```

441

## (2) INFORMATION ON SEQ ID NO. 25:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 1131 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:

09673400.122700

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

```

cgggaggtga aatccggttc taaccgggtcc gggggtccca gcgctataaa aacttttataa 60
acccccccgga gcccgagcag tctgaagaag aggcgagaac gacccccgga ccgaccaaaag 120
cccgcgcgcc gctgcacccc gcgtccagca cctacgtccc gctgccgtcg ccgcgcgccac 180
catgcccaag aqaaaagctg aaggggatgc taaggagat aaagcaaaag tgaaggacga 240
accacagaga agatcccgga ggtgtctgc taaacctgct cctccaaaag cagagcccaa 300
gcctaaaaag gccccctgcaa aqaagggaga gaaaggtacc aaagggaaaa agggaaaaagc 360
tgatgtctgc aaggagggga ataacccctgc aqaaaatgga gatgccaaaa cagaccaggc 420
acagaaagct gaaggtgctg gagatgccaa gtgaagtgtg tgcatTTTTTg ataactgtgt 480
acttctgggt actgtacagt ttgaaatact attttttatc aagttttata aaaatgcaga 540
tttttgtttt actttttttt ttttttttaa agctatgttg ttacacacac gaacacttca 600
ttgttgtttt tgggggaagg ggcataatgt actaatagaa tgtctccaaa gctggattga 660
tgtggagaaa acacctttcc ctctctagtt tgagagactt cctcttgctt cccaggagga 720

```

```

gggattccct gactttgaca cacatggcca cttgggcaca aaagccttgt ggtatagaaa 780
aacaaaatttg ttttatgtc ctcttctccc tttccattt tcagcataga ctttaactccc 840
ttaagcccaag acatctcttg agacctgacc cctagtccat ggttacccag gtgtcaggca 900
atctggactt tccagtgatg ccactgagat ggcacccgtc aaaagagcag tgggtccatt 960
ctcagatttg ggaacttccag ataaattctg ccattttcat ttCactttct gaaagtCagg1020
gtcggcttgt gaaaagtgtt taaacaacat gctaaatgtg aaatgtcaac cctcactctal1080
aaacttttcc ctgggtcaga ggatccgatg gaggacttca attggggggt t 1131

```

## (2) INFORMATION ON SEQ ID NO. 26:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1071 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

00673400.122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

```

gtacctccaa agacagagac accaagaaga atcggaacat acaggctttg atatcaaagg 60
tttataaagc caatactctg gaaagagaaa accgtgagac ttccagatct tctctgggtga 120
agtgttgttt cctgcaacga tcacgaacat gaacatcaaaa ggatcgccat ggaaagggtc 180
cctcctgctg ctgctgggtg caaacctgct cctgtgccag agcgtggccc ccttgcccat 240
ctgctcggcg ggggctgccc gatgccaggt gacccctcga gacctgtttg accgcggcgt 300
cgctcctgcc cactacatcc ataacctctc ctccagaaatg ttccagcgaat tcgataaaacg 360
gtatacccat ggcggggggg tcattaccaa ggccatcaac agctgccaca ctctctccct 420
tgccaccccc gaagacaagg agcaagcccc acagatgaat caaaaagact ttctgagcct 480
gatagtcagc atattcgcat cctggaatga gccctctgat catctgggtca cggaaagtacg 540
tgggtatgcaa gaagccccgg aggcctatcct atccaaagct gttagagatcg aggaagcaaac 600
caaacgggctt cttagagggca tggagctgat agtcagccag gttcatcctg aaaccaaaga 660
aaatgagatc taccctgtct ggtcgggact tccatccctg cagatggcgtg atgaagagtc 720
tcgcctttct gcttattata acctgctcca ctgccctacgc agggattcac ataaaatcga 780
caactatctc aaqctcctga agtgccgaat catccacaac aacaactgct aagcccacat 840
ccatttcctc tactttctgag aaggttcctta atgattcgtt ccattgcaag ctctcttttag 900
ttgtatctct ttgtaatcca tgcctgggtg taacagggtct cctcttaaaa aataaaaaact 960
gactcctttg agacatcaaa atctaaaaaa accttaatggg ccgggcgcag tggctcatgg 1020
ctgtggtccc ggcactcttg gaggcgaggg caggcgggatc aggaaggtcag g 1071

```

## (2) INFORMATION ON SEQ ID NO. 27:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 896 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

007221-0042800

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

```

gtgacccggct cagaccgggt ctggagacaa aaggggcccg gccggccgga gggggaacgg 60
ccggggccggg gaggggagcga agagcgccgg cagcgagcga gatgcagcac cgaaggcttcc120
tcccctccac cctcccgcgc ctgctggcgc tcacctccgc ggtccgcaaa aagaagaata180
aggtgaagaa gggcgccggc gggagcgagt gcgctgagt ggccctgggg ccctgccacc240
ccagcagcaa ggaattgcgg cggggtttcc gcgagggcac ctggcgggcc cagacccagc300
gcacccgggt cagggcgccc tgcacctgga agaaggagtt tggagccgac tgcaggtaca360
agctttgaaa ctgggtgctg tgtgatgggg gcacaggcac caaagtcggc caaggcacc420
tgaagaaagg gcgctacaat gctcagtgcc agggagccat ccgctgtcac aagcccttgc480
cccccaagac caaagcaaat gccaaagcca agaaagggaa gggaaaggac tagacgccaa540
gccttgatgc caaggagccc ctgggtgtac atggggcctc gccccagccc tccccctccc600
aggcccgaga tgtgacccac cagtgccttc tgtctgctcg ttactcttaa tcaatcatgc660
ccctgccttg cctctcact ccccagcccc acccctaagt gcccaaatg gggaggagca720
agggattctg ggaagcttga gcctccccca aagcaatgtg agtcccgag ccgcctttt780
tcttccccca caattccatt actaagaaac acatcaata aactgacttt tccccccaa840
aaaaagctct tcttttttaa tataaaaaaa aaaaaaaaaa aaaaaaaa 896

```

## (2) INFORMATION ON SEQ ID NO. 28:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1050 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

```

ttttctattt tttttttttt tttttctcag ttcaagttaa atacaaacta caaaagacta 60
atgggttgct ctactaatat atcatataaa ccagtagcct gccacacact ccaactcagg 120
ccattctcat caaagggaaga aaggctcggtc tctccacccc ctgtaggaaa ggccctgcct 180
gtaagacacc acaattcgcc tgaatctgaa gtcttggttt ttactaatgg aaaaaaaaaa 240
tcagagaagg gtttttctct catggctgccc caccgcagcc tggcactaaa acagcccagc 300
gtccactctc gctctggaaa atattctttg ctcttttgg gatcaggtt gatggtatca 360
ctgcccaggt ttccagccagc tgggcacact tcccctatgt tgcctgtgaa ctggagagcc 420
tgaactagtc tcaaaagtct atccacagag cggccaaacag ggaggtcatt taccagtgat 480
tgcggaagaa tacctttatc atcaatgata aaaaaggccc tgaacgagat gccttcacca 540
gcctttaaag cccataatc ctgagcaaat gtcgcgcttc ggctctgata caaagggaatg 600
ttctatgggt ccagtcctcc tgtcttctta ggtgtattga cccatgtcag atgacagaa 660
tgagaattcca cagaagcacc aatcactttg cagttgagtt tcttaaatct ttctgcctca 720
atctgaaag caatgatctc cggggggcac acaaagggtga agtcaagagg gtaaaaaga 780
aacacacact attctctttt gtagtcagac aggcctgatar ctttaaacct accatctggc 840
ataacagctg tggctctgaa gttgggggca ggggtgcocaa ttttagcatt tcttgaagac 900
atcttccatc cagcagctccc aacacaagtc gcagaaacta accaccgaca ccaggcaaga 960
acaagacgcg caagagctct cggggcgct gcctttatag ccagtaggga tctcgccacal020
gtcggaaacgg acgggggtgc cggagtagga 1050

```

00221.004E7960



## (2) INFORMATION ON SEQ ID NO. 29:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 581 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

caggcttctt tctggcaaca ggctgtgggtc acgctctcgc tgggtctttc tgcgcgccatc 60  
 ttggttccgc gttccctgca caaatgccc gccgaacacc agaaaccgtc cctgctacag120  
 agcaggagtt gccgcagccc caggctgaga cagggtctgg aacagaatct gacagtgatg180  
 aatcagtaac agagcttgaa gaacaggatt ccaccaggc aaccacacaa caagcccagc240  
 cggggcagc agctgaaatc gatgaagaac cagtcagtaa agcaaaacag agtcggagtg300  
 aaaagaaggc acggaaggct atgtccaaac tgggtctctc gcagggtaca ggagttacta360

gagtcactat ccggaaatct aagaatatcc tctttgtcat cacaaaacca gttgtctaca420  
 agagccctgc ttcatagatc tacatagttt ttggggaagc cagatcgaag attatcccag480  
 caagcacaa ctagcagctgc tgagaagtca agttcagggt aactgtctca acgttcagga540  
 aacccccggc ttccactgta gagggggagc aaggggaggg t 581

## (2) INFORMATION ON SEQ ID NO. 30:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 264 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN

09673400.122700

## (C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

```

gggaactatgt tctgagccctg cgaagaagt ttgtgtggg actgtgggca gtgaatgcgt 60
tgggaacaat atggaaaaat gggagctgcc ctcagttct ccccaagtgt gactcacttt 120
cgggggtgtcc caaaagccctg attccagggc ctgctagccc gacccccggtg acgcctccac 180
ccgcgccttg ccccagcctt caccgcgat cgcgcgcctc cggggcacac cctccgcag 240
aaaaacagccg gcggcgccgcg agac 264

```

## (2) INFORMATION ON SEQ ID NO. 31:

## (i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 111 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

```

cggcgaatca cttataaatg gcgcggaagc aggagcccca aggcataatt gcaggagggg 60
tgagcgaaatg ctgtgcttcc atgggcctct tacgttgatg aggcataagta t 111

```

## (2) INFORMATION ON SEQ ID NO. 32:

## (i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 76 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

002221-0042790

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

PFCEETKTIER LWPRCRPPAA VGFSTQNPGV GDESNLFSL PFLGSKANPI PTHWSSALIF60  
NLPSPPFQNT HIPFQN 76

(2) INFORMATION ON SEQ ID NO. 33:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 72 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

SSFLFSFQTQ FHKNRKDKVF SSRQAKPFPH HQSILKIHEE VERSVSGALK GSSSSNPTAA60  
EKIEIEILKI TS 72

(2) INFORMATION ON SEQ ID NO. 34:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 70 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

KKLOYFCAEI KNSHCKTKIK LAQIRKPGGA KCQVSKVHFF SLSKRSSTKT ARIKFSVADK60  
QSPFHINQS 70

002221.0042260

## (2) INFORMATION ON SEQ ID NO. 35:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 60 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

SSGPAPGCSP FAGTRKNFPS MVLERTFLK INYIFLCIPM EFQFIRCSPW PPQNTTEVIPA60

## (2) INFORMATION ON SEQ ID NO. 36:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 63 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

ASGVHTETHR YNLLSAKSRK KGWGYLGWLG FDFLLVCLFC TKTVLSFEYR RDISIYMLSN60  
QDG 63

## (2) INFORMATION ON SEQ ID NO. 37:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 170 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

09673400.122700

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

AAAAAAQTPT HLTLPADLQT LHLNRPTLSF ESKLEWNNDI PEVNHNLNSEH WRKTEKWTGH 60  
EETNHLETDF SSGDMTELEL GPSRLQPIR RHPKELPOYG GPGKDIFEDQ LYLPHVSDGII20  
SVHQMTMAT AEHRSNSIA GKMLTKVEKN HEKERSQHLE GSASSLSDD 170

(2) INFORMATION ON SEQ ID NO. 38:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 144 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

ARAPTDMRF RRRLSADPHA TQRNSAEARG TMDGRVQLMK ALLAGPLRPA ARWRNPPIF 60  
PETFDGQDOR LPEFIVQTCS YMEVDENTFS NDALKVTFLI TRLTGPALQW VIPYIRKES9120  
LLNDYRGFLA EMKRFGWEE DEF 144

(2) INFORMATION ON SEQ ID NO. 39:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 178 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

HSLGRAPVET LAVATGTANS SQSTRPOARG SPGLEVLVLL PSKDSLHLGQ KAPVIEQGA 60  
LLPDVGDHPL QGWPREAGDE ERHLQGVVGE RVLVHEHVGA RLHDELRESV GISVKRLGKG120  
NRVPFATRGR PEGPGQEGELH QLHPTVHRAA RLRGVSILGCV GVSAKASPEA HVEGGGPG 178

002221-004E7560

## (2) INFORMATION ON SEQ ID NO. 40:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 89 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN

- (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

KLTIQINTGCR NMLALCIRGH AQIQEIYLA TFSRKGTLGI IRVILEVFLG FFFFLRQSC60  
 CIAQAGSVVA QSQLIASSIT QGLSNPPTL 89

## (2) INFORMATION ON SEQ ID NO. 41:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 95 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN

- (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

IVTWKRVFMS LCQRPPFFVR IGIFRLKGL AHIRCDLFIP VVMEGHICQS LESAKAGTRF60  
 PGFQNGCANP RELGCKFVKN QHHVWQLSIG ARSLP 95

## (2) INFORMATION ON SEQ ID NO. 42:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 154 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

00673400.122700

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

CQLVFRIQTD GSYWSLGLTS SGNITFSWAE MLLPALKQHS VLKTSWQAPG SNTQLPNMML 60  
ILHEFATQFS RVCTSPPLWAG EPGFGLRLRLQ ALADVALHNN GNEKVTFYVR QALKESEKPN120  
PHKRRGT'LAK THGNFPFNSD LDRRATQDSF SCSV 154

(2) INFORMATION ON SEQ ID NO. 43:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 79 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

LATILGVETC LPYVSEDMLS RSKRYIWQLF LEKAHWVSFI TFLSFFGFFF FFFETVLLYC60  
PGWSVVAQSQ LIASSITQA 79

(2) INFORMATION ON SEQ ID NO. 44:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 82 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

CQLVFRIQTD GSYWSLGLTS SGNITFSWAE MLLPALKQHS VLKTSWQAPG SNTQLPNMML60  
ILHEFATSWL FRLQHSVAVGT QS 82

002221.00422960

## (2) INFORMATION ON SEQ ID NO. 45:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 68 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

RGSKDRNSGQ GSGSYGQLSC RGFSQFQSRV CTFPLWAGEF GPGLRRLQAL ADVALHNNNGN60  
 EKVTPYYVR 68

## (2) INFORMATION ON SEQ ID NO. 46:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 87 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

DYVVSRLRKKF VWGLWAVNAL GTIWKIGSCP QFLPKLOSLS GCPKSLIPGP ASPTPVTPPP60  
 APGPSLHPRS PFSGAHPPPE NSRRAAR 87

## (2) INFORMATION ON SEQ ID NO. 47:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 51 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

002227.0042980



- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

QALESQFWDI PKVSPTWGET EGSSQFSILF PTHSLPTVPT QTSFAGSQHS P

51

(2) INFORMATION ON SEQ ID NO. 48:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 20 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

RRITYKWRRS RSPKAKLQEG

20

(2) INFORMATION ON SEQ ID NO. 49:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 36 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

GESLINGAEA GARRLNCRRG ERMLCFHGPL TLMRQS

36

09673400-122700

## (2) INFORMATION ON SEQ ID NO. 50:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 26 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

KHSIRSPLLQ FSLRAPASAP FISDSP

26

## (2) INFORMATION ON SEQ ID NO. 51:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 25 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

EAHESTAFAH FSCNLAFGLL LRRHL

25

## (2) INFORMATION ON SEQ ID NO. 52:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 3665 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

002221.00462960

- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

GGCCATTG TGAAGAGAGG AAGACTGAGC GSTTGCGGC GCSTTGCGCA CCTCCAGCAG 60  
 CAGTGGGCTT CTCTACGCAG AACCCGGGAG TAGGAGACTC AGAAATCGAA TCTCTTCTCC 120  
 CTCCCTCTCT TGGGCAGCAA GGCGAACCCC ATCCCTACTC ACTGGAGCTC AGCTTTGATT 180  
 TTTAACCTCC CTTCGCCACC CTTCAGAAC ACACACATTC CATTCAAAA CTGATTTTAT 240  
 AAAGACATTT TAAACATAAT GATGCAACTT GGTGTGCACT ACAGCAAAATG TACAGGTGTT 300  
 TTTTCTTTAA TTGTTTCCAA AACCCGGGACC TGGATTTAAG ATGTAATTTT TAAAAATTTCT 360  
 ATTTCTATTT TTTCTGCAGC AGTTGGGTTA GAGGAGGAGG AGCCTTTTAG CCTCTCATAA 420  
 ACTGACCTCT CTACTTCCTC GTGTATTTT AAGATTGATT GATGATGTGG AAAGGGCTTT 480  
 GCTTGCTGCG TACTGAAAC TTTATCTGCG GSTTTTGTG GAAACTGCTT TTGGAAGAG 540  
 AAAAGAAATG AACTTTACTG ACTTGACATT TTTGCACCTC CCGTTTTTCT AATCTGGGCT 600  
 ATTTTATTTT TTGTTTTTTT ACAGTGAGAT TTTTGTGATC TTCAGCTTAC ATTTCTGGGG 660  
 TTTGTGAGGA AACCTTTACC CATCAACAC GATGGCCGCG AACGTTACCA ACAAGACAGA 720  
 TCTCGCTCC ATGAACCTCC GTGTATTCAT TGGGAATCTC AACACTCTTG TGGICAAGAA 780  
 ATCTGATGTG GAGGCAATCT TTTGGAAGTA TGGCAAAATT GTGGGCTGCT CTGTTCATAA 840  
 GGGCTTTGCC TTCTTTCAGT ATGTTAATGA GAGAAATGCC CGGGCTGCTG TAGCAGGAGA 900  
 GGATGCGAGA ATGATTGCTG GCCAGGTTTT AGATATTAACT CTGGCTGCAG AGCCAAAAAT 960  
 GAACCGAGGA AAAGCAGGTG TGAACGATC TGCAGCGGAG ATGTACGGCT CCTCTTTGA1020  
 CTTGCACTAT GACTTTCAAC GGGACTATTA TGATAGGATG TACAGTTACC CAGCACGTG1080  
 ACCTCCTCCT CCTCCTATTG CTCGGGCTGT AGTGCCCTCG AACCTCAGC GTGTATCAGG1140  
 AAACACTTCA CGAAGGSGCA AAAGTGGCTT CAATTCTAAG AGTGACAGC GGGGATCTTC1200  
 CAAGTCGGA AAGTTGAAG GAGATGACCT TCAGGCCATT AAGAAGGAGC TGACCCAGAT1260  
 AAACACAAAA GTGGATTCTC TCCTGGAAAA CCTGGAAAA ATTGAAAAGG AACAGACAA1320  
 ACAAGCAGTA GAGATGAAGA ATGATAGTC AGAAGAGGAG CAGAGCAGCA GCTCCGTGAA1380  
 GAAAGATGAG ACTAATGTGA AGATGGAGTC TGAGGGGGGT GCAGATGACT CTGCTGAGGA1440  
 GGGGACCTTA CTGGATGATG ATGATAATGA AGATCGGGGG GATGACCAGC TGGAGTTGAT1500  
 CAAGGATGAT GAAAAAGAGG CTGAGGAAGG AGAGGATGAC AGAGACAAGG CCAATGGCGA1560  
 GGATGACTCT TAAGCACATA GTGGGTTTTA GAAATCTTAT CCCATTATTT CTTTACCTAG1620  
 GCGCTTGCTT AAGATCAAA TTTTCACGAG ATCCTCTCCC CTAGTATCTT CAGCACATGC1680  
 TCACTGTCTT CCCCATCTTT GTCTTCCCA TGTTCACTAA TTCATATTGC CCCGCGCTA1740

08673400-122700

GTCCGATTTT CACTTCTCTT GACGCTCCTA GTAGTTTGT TAAGTCTTAC CCGTGAATTT1800  
 TTGCTTTTAA TTTTGATACC TCTTTATGAC TTAACAATAA AAAGGATGTA TGGTTTTTAT1860  
 CAACTGCTCT CAAAATAATC TCTTGTTATG CAGGGAGTAG AGTTCTTTTC ATTCATACAT1920  
 AAGTTCAGTA GTTGCTTCCC TAACTGCAAA GGCAATCTCA TTTAGTTGAG TAGCTCTTGA1980  
 AAGCAGCTTT GAGTTAGAAG TATGTGTGTT ACACCTCTAC ATTAGTTGAG TGTGTGGGGC2040  
 AGTTCAACAC AAATGTAAAC ATGTATTTT GTGAATGAGA GTTGGCATGT CAAATGCATC2100  
 CTTAGAAAAA ATAATTAGTG TTATAGTCTT AAGATTGTTT TCTTAAAGTT GATACGTGGG2160  
 GTTATTTTTG TGAACAGCCT GATGTTTGGG ACCTTTTTTC CTCAAAATAA ACAAGTCTT2220  
 ATTTAAACCG GAAATTTGGG AAAAAAATAA AAAAAAATTT TTTATTTTTG TATTTTATTA2280  
 TTGTTTACTT CAAACTTTGT TTTACAGCGT CCTCCACAAA ACCTCTAGAA TGCACATAGAT2340  
 ATATTTTTCT TGGAGTCATA ATCATGATGC ATACCAACAC AACACTACTC AAATTATATT2400  
 TCATGTAGAT GCATGTTTGA TTAGAGGAGT AACCTTGACAT AGAGTGGAGA CTTTTTCAA2460  
 ATGGCTTTTA CATCCTAATG AAAGTTTGGG AAGTATATCC TCTCTGCCCT TTGATCAGTG2520  
 CTTTGTGGTC CAGCTGGCAC CCTTCTGAG GTTTGTGTTT TGTGCTAAAT GGTTTTGTCC2580  
 TTAATAGGA GAGGCTCAAA AACATCARGA TTTGAGGAAA ATGGCGACAC TGGCATAATG2640  
 GAACGCCCTC GCTTCTATTT TGTCTTTTAA ATTACTATTT ATAGCCCCAG TTACCTCTGT2700  
 AATTCGGAAG TGTATATACC TCCATGTTCC TGAAAAAAG AAAACTCTTA CTTCCTGATA2760  
 TTCCATAGAC TGCCTTCCCA GGTGATTGAG AACATAGAGA ATGTTACACA TTTATTTTAC2820  
 TCTAAATGAT CTTTTACCCC TGTTAGCTAA TCTTTGTGTT TTGCTCAACT TTAATTAA2880  
 CAGTGATTGC ATTTTTAGCA TCCAGTTGTA AGATGAATAT ATTTAAACAG TACGAGTGT2940  
 GGTGATACCT CATCCTTGAA AGGCTTAGTT CATTTGTGTT TTATACTTGA GTTTTTCAG3000  
 CATAGCAGAA AATGCCGCTT ATAATTTTTG TGCACACAAA CTTTGGAAAT CCCCTGTAAA3060  
 GTTGCTATGG TTTCTATGCA TGCGGCAGCT GCCCTTTTTT CATCCCACCT ATTACAGGCA3120  
 AAACCCATGT CTTATTATG AGGATTTTAT AGATCATTTT CTGTAAACAG TGACAAAAGC3180  
 AGAAAAAGT GAAGAGGCTG AAGTATGAAC TACCCTTGGA GCCCATATAC ATGATATAGG3240  
 CAATTTCTTT TGATGTTTAA TTAGCTCAAA AATACTACCC ACTTGATGTT TTCTAATCTG3300  
 ATGTAGCTC ATGTTTACACA GACTTTTGTG AAGTAAACCG TGACTAGAAA ATAAACTGGA3360  
 TGCTTAGGAG AGAGTGTGAG ATGTATAAGA TGCTAAATAA ACCTGTTTAA TATTATGTT3420  
 AGCTGAAGT TTTTGGGAAA TACTGAACAA ATTAGTCCAC AATCAAGTGT CTACTTTTC3480  
 CTTCACTGTA GGGGCTCTCC CTGCACAGAG CAGTCTGTTT AGCTGTGAAC ACCACAATCT3540  
 CGAGATGTTT AAGTCCCTTA CATAAAATGG CATAGTATTT ATATGTAAAC TTGCAATATT3600  
 CTCCTGTATA TTTTAAATCA TCTCTACATT AAAATACCTG ATAAAACTTA AATAAAAAAA3660  
 AAAAA 3665

## (2) INFORMATION ON SEQ ID NO. 53:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 301 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

GNLYPSNTMA SNVTNKTDPR SMNSRVFIGN LNTLVVKKSD VEAIFSKYKG IVGCSVHKGF 60  
 AFVQYVNEIN ARAAVAGEDG RMIAGQVLDI NLAAEPKVN R GKAGVKRSAA EMYGSSFDLD120  
 YDFQRDYDR MYSYPARVP PPIIARAVVP SKRQRVSGNT SRRKSGFNS KSGQRGSSK180  
 GKLGDDLLQA IKKELTQIKQ KVDSELENLE KIEKEQSKQA VEMKNDKSE EQSSSSVKKD240  
 ETNVKMESEG GADDSAEEDG LDDDDDNEDR GDDQLELIKD DEKEAEEDG DRDKANGEDD300  
 S 301

09573403.122700

## (2) INFORMATION ON SEQ ID NO. 54:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 112 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

EGSSPLALSL SSSPSSASFS SSLINSSWSS PRSSLSSSSS RSPSSAESSA PPSOSIFTLV 60  
 SSFFTELLLC SSSDLSFFIS TACLLCSFSI FSRFSRREST FCFINWVSSEL MA 112

## (2) INFORMATION ON SEQ ID NO. 55:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 107 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

TRNLEKKKKK NFLFLYFIIV YFKLCFTASS TKPLECTRYI FLGVIIMMHT NTTLLKLYFI 60  
 EMHVALRSQI DIEWRLFQNG FYILMKVWEV YPLCLFISAL WSSWHFF 107

00673400-122700

WO 99/54448

PCT/DE99/01178

**Claims**

1. A nucleic acid sequence that codes a gene product or a portion thereof, comprising

- a) a nucleic acid sequence, selected from the group Seq. ID Nos. 14-18, 30, 31, and 52,
- b) an allelic variation of the nucleic acid sequences named under a)

or

- c) a nucleic acid sequence that is complementary to the nucleic acid sequences named under a) or b).

2. A nucleic acid sequence according to one of the sequences Seq. ID Nos. 14-18, 30, 31, 52, or a complementary or allelic variant thereof.

3. Nucleic acid sequence Seq. ID No. 1 to Seq. ID No. 31 and Seq. ID 52, characterized in that it is expressed elevated in hysteromyomic tissue.

4. BAC, PAC and cosmid clones containing functional genes and their chromosomal localization according to sequences Seq. ID No. 1 to Seq. ID No. 31 and Seq. ID 52 for use as vehicles for gene transfer.

5. A nucleic acid sequence according to claims 1 to 4, wherein it has 90% homology to a human nucleic acid sequence.

6. A nucleic acid sequence according to claims 1 to 4, wherein it has 95% homology to a human nucleic acid sequence.

00577400-123700

7. A nucleic acid sequence comprising a portion of the nucleic acid sequences named in claims 1 to 6, in such a sufficient amount that they hybridize with the sequences according to claims 1 to 6.

8. A nucleic acid sequence according to claims 1 to 7, wherein the size of the fragment has a length of at least 50 to 4500 bp.

9. A nucleic acid sequence according to claims 1 to 7, wherein the size of the fragment has a length of at least 50 to 4000 bp.

10. A nucleic acid sequence according to one of claims 1 to 9, which codes at least one partial sequence of a bioactive polypeptide.

11. An expression cassette, comprising a nucleic acid fragment or a sequence according to one of claims 1 to 9, together with at least one control or regulatory sequence.

12. An expression cassette, comprising a nucleic acid fragment or a sequence according to claim 11, in which the control or regulatory sequence is a suitable promoter.

13. An expression cassette according to one of claims 11 and 12, wherein the DNA sequences located on the cassette code a fusion protein, which comprises a known protein and a bioactive polypeptide fragment.

14. Use of nucleic acid sequences according to claims 1 to 10 for producing full-length genes.

15. A DNA fragment, comprising a gene, that can be obtained from the use according to claim 14.

09673400.122700

16. Host cell, containing as the heterologous part of its expressible genetic information a nucleic acid fragment according to one of claims 1 to 10.

17. Host cell according to claim 16, wherein it is a prokaryotic or eukaryotic cell system.

18. Host cell according to one of claims 16 or 17, wherein the prokaryotic cell system is E. coli, and the eukaryotic cell system is an animal, human or yeast cell system.

19. A process for producing a polypeptide or a fragment, wherein the host cells according to claims 16 to 18 are cultivated.

20. An antibody that is directed against a polypeptide or a fragment that is coded by the nucleic acids of sequences Seq. ID Nos. 1-31 and Seq. ID 52, which can be obtained according to claim 19.

21. An antibody according to claim 20, wherein it is monoclonal.

22. An antibody according to claim 20, wherein it is a phage display antibody.

23. Polypeptide partial sequences according to sequences Seq. ID Nos. Seq. 32-51 and Seq. ID Nos. 53-55.

24. Polypeptide partial sequences according to claim 23, with at least 80% homology to these sequences.

25. A polypeptide that is known from a phage display and that can bind to the polypeptide partial sequences according to claim 23.

09573440.122700



26. Polypeptide partial sequences according to claim 23, with at least 90% homology to these sequences.

27. Use of polypeptide partial sequences according to sequences Seq. ID Nos. 32 to 51 and Seq. ID Nos. 53-55 as tools for finding active ingredients against hystero myoma.

28. Use of nucleic acid sequences according to sequences Seq. ID Nos. 1-31 and Seq. ID No. 52 for expression of polypeptides that can be used as tools for finding active ingredients against hystero myoma.

29. Use of nucleic acid sequences Seq. ID Nos. 1-31 and Seq. ID No. 52 in sense or antisense form.

30. Use of polypeptide partial sequences Seq. ID No. 32 to Seq. ID No. 51 and Seq. ID Nos. 53-55 as pharmaceutical agents in gene therapy for treatment of hystero myoma.

31. Use of polypeptide partial sequences Seq. ID No. 32 to Seq. ID No. 51 and Seq. ID Nos. 53-55 for the production of a pharmaceutical agent for treatment of hystero myoma.

32. Pharmaceutical agent, containing at least one polypeptide partial sequence Seq. ID No. 32 to Seq. ID No. 51 and Seq. ID Nos. 53-55.

33. A nucleic acid sequence according to claims 1 to 10, wherein it is a genomic sequence.

34. A nucleic acid sequence according to claims 1 to 10, wherein it is an mRNA sequence.

35. Genomic genes, their promoters, enhancers, silencers, exon structure, intron structure and their splice variants, that

00673400.122700

can be obtained from cDNAs of sequences Seq. ID No. 1 to Seq. ID No. 31 and Seq. ID 52.

36. Use of the genomic genes according to claim 33, together with suitable regulatory elements.

37. Use according to claim 36, wherein the regulatory element is a suitable promoter and/or enhancer.

38. A nucleic acid sequence according to claims 1 to 7, wherein the size of the fragment has a length of at least 300 to 3500 bp.

03673400.427403

1/10

## Systematic Gene Search in the Incyte LifeSeq Database

Normal tissue  
~50,000 individual ESTs

Tumor tissue  
~50,000 individual ESTs

## Priority list

## High

Prostate  
Breast  
Ovary  
Bladder  
Uterus

Iterative assembling  
with  
increasing mismatch

## Low

~8,000 contigs  
+  
~25,000 individual  
sequences

~8,000 contigs  
+  
~25,000 individual  
sequences

## Comparison of databases

normal tissue-  
specific  
(expected: 100-500)

nonspecifically  
expressed genes

tumor tissue-  
specific  
(expected: 100-500)

## Genes of Interest

Figure 1

REPLACEMENT PAGE (RULE 26)

00224.0442300

## Systematic Gene Search in the Incyte LifeSeq Database

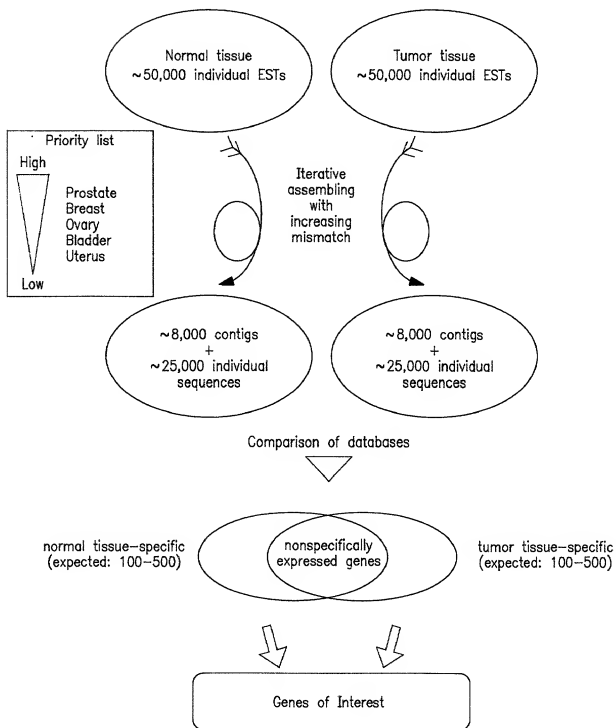


FIG. 1

## Principle of EST Assembly

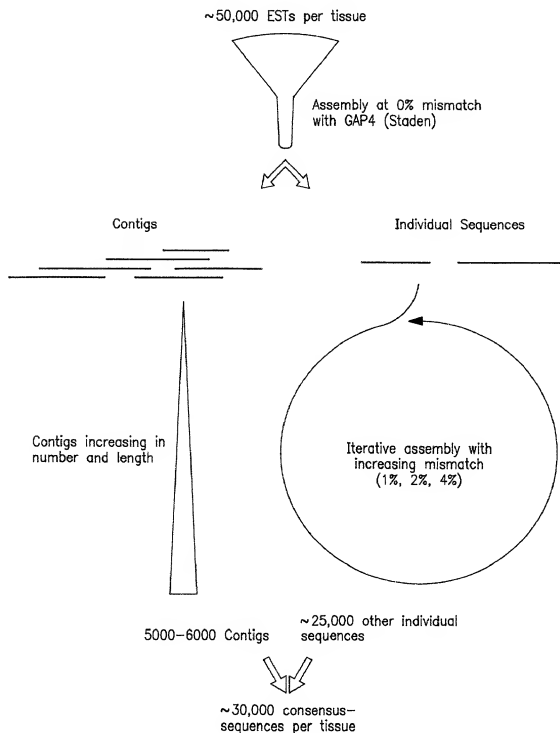


FIG. 2a

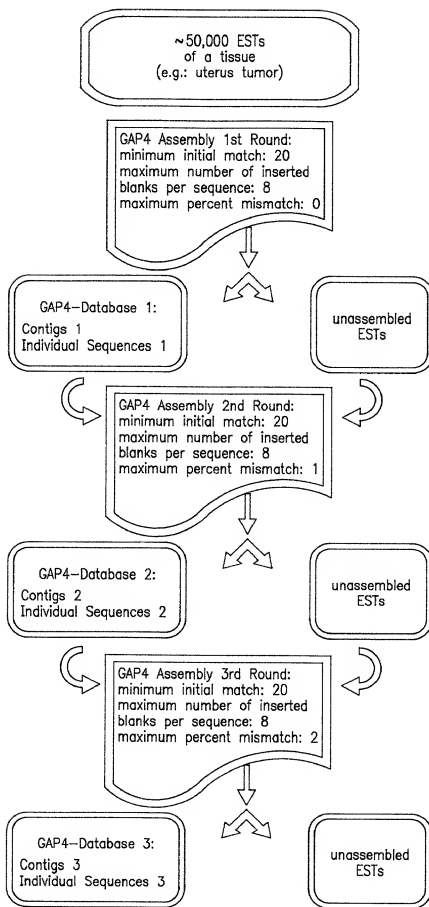


FIG. 2b-I

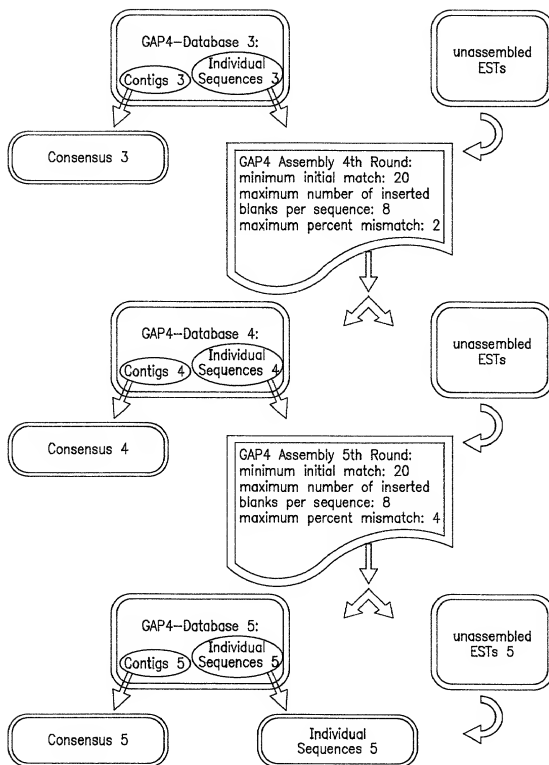


FIG. 2b-2

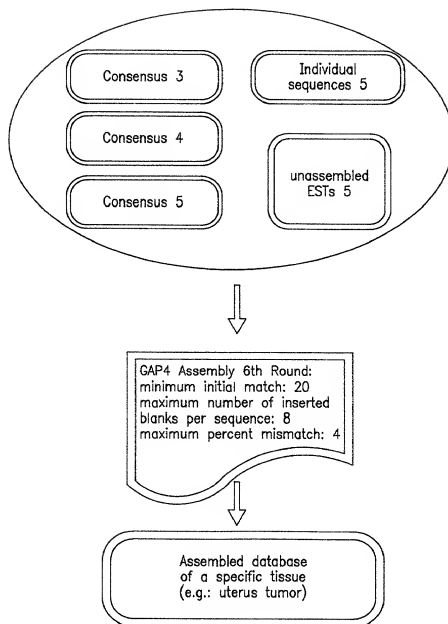


FIG. 2b-3



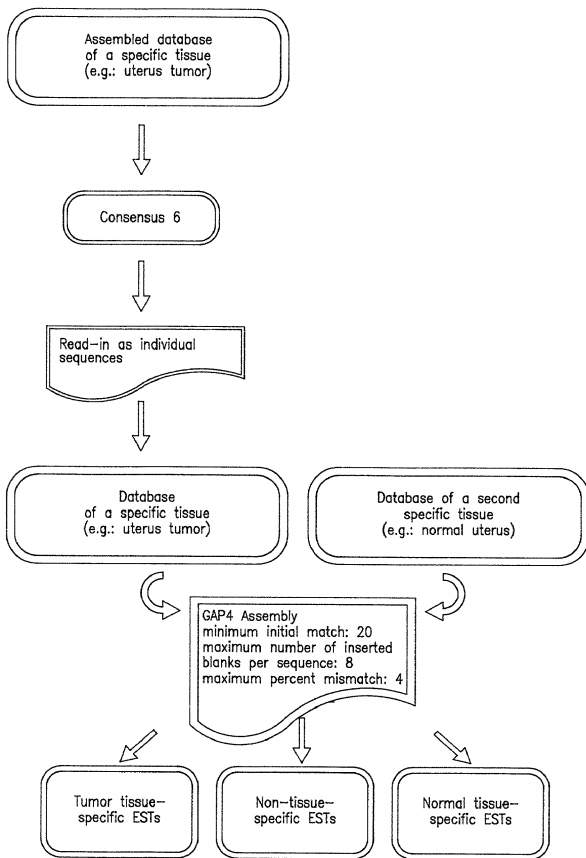
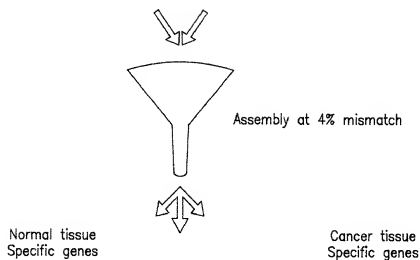


FIG. 2b-4

In silico subtraction of gene expression in various tissues

~30,000 consensus sequences  
normal tissue

~30,000 consensus sequences  
tumor tissue



Genes expressed in both tissues

FIG. 3

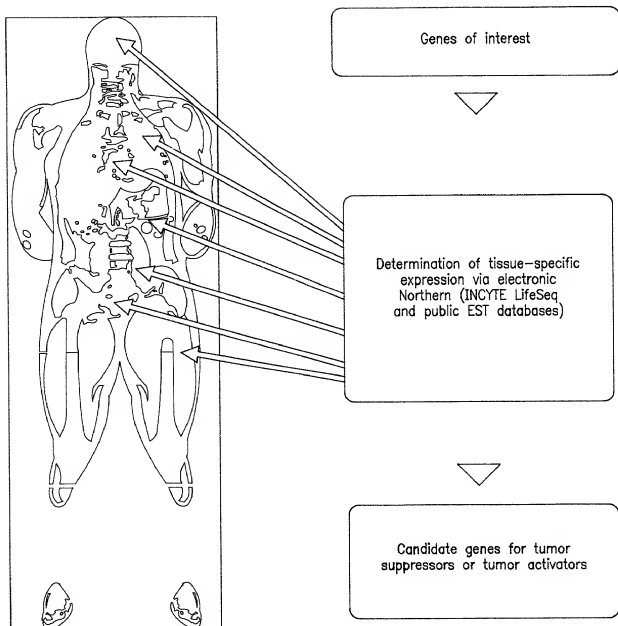


FIG. 4a

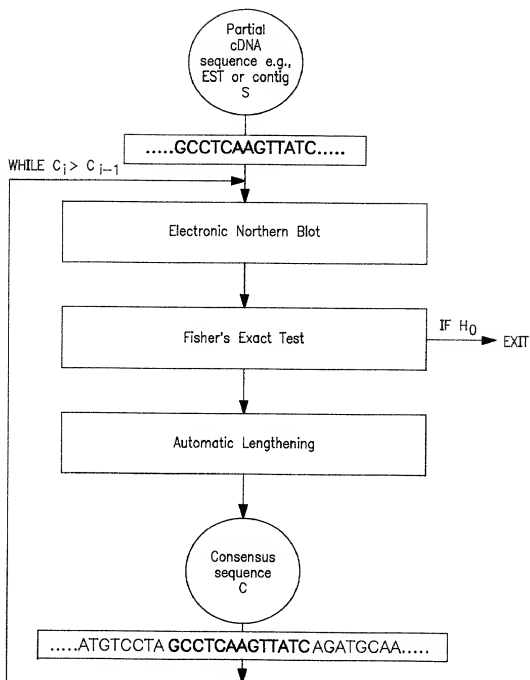


FIG. 4b

Isolation of genomic BAC and PAC clones



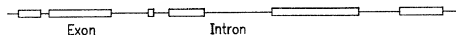
Chromosomal clone localization via FISH



Hybridization signal



Sequencing of clones that are located in regions that have chromosomal deletions in prostate and breast cancer leads to identification of candidate genes



Confirmation of candidate genes by screening of mutations and/or deletions in cancer tissues

FIG. 5

Attorney Document Number:

SCH 1779

**DECLARATION FOR PATENT APPLICATION**

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name.

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

**HUMAN NUCLEIC ACID SEQUENCES OF UTERUS MYOMA TISSUE**

the specification of which

☐ is attached hereto

☒ was filed on 15 April 1999 as United States Application Number or PCT International Application Number PCT/DE99/01178 and (if applicable) was amended on \_\_\_\_\_

I hereby authorize our attorneys to insert the serial number assigned to this application.

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR §1.56.

I hereby claim foreign priority benefits under 35 U.S.C. §119(a)-(d) or §365(b) of any foreign application(s) for patent or inventor's certificate, or §365(a) of any PCT International application which designated at least one country other than the United States, listed below and have also identified below, by checking the box, any foreign application for patent or inventor's certificate, or PCT International application having a filing date before that of the application on which priority is claimed.

PRIOR FOREIGN/PCT APPLICATION(S) AND ANY PRIORITY CLAIMS UNDER 35 USC §119			
APPLICATION NO.	COUNTRY	DAY/MONTH/YEAR FILED	PRIORITY CLAIMED
198 17 947.2	Germany	17 April 1998	X

I hereby claim the benefit under 35 U.S.C. §119(e) of any United States provisional application(s) listed below.

PROVISIONAL APPLICATION(S) UNDER 35 U.S.C. §119(e)	
APPLICATION NUMBER	FILING DATE

I hereby claim the benefit under 35 U.S.C. §120 of any United States application, or §365(c) of any PCT International application designating the United States, listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT International application in the manner provided by the first paragraph of 35 U.S.C. §112.

I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR §1.56 which became available between the filing date of the prior application and the national or PCT International filing date of this application.

PRIOR U.S./PCT INTERNATIONAL APPLICATION(S) DESIGNATED FOR BENEFIT UNDER 37 U.S.C. §120		
APPLICATION NO.	FILING DATE	STATUS — PATENTED, PENDING, ABANDONED

I hereby appoint the following attorney(s) and/or agent(s) to prosecute this application and to transact all business in the Patent and Trademark Office connected herewith: I, William Millen (19,544); John L. White (17,745); Anthony J. Zelano (27,969); Alan E.J. Branigan (20,565); John R. Moses (24,983); Harry B. Shubin (32,004); Brion P. Heaney (32,542); Richard J. Traverso (30,595); John A. Sopp (33,103); Richard M. Lebovitz (37,067); John H. Thomas (33,460); Nancy J. Axelrod (44,014); James E. Ruland (40,921) and Jennifer J. Branigan (37,432)

14

Declaration for Patent Application (Continued)

**Correspondence Address:**  
**MILLEN WHITE ZELANO & BRANIGAN, P.C.**  
 Suite 1400  
 2200 Clarendon Boulevard  
 Arlington, VA 22201  
 TEL (703) 243-6333  
 FAX (703) 243-6410

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

1-00 Full Name of sole or first inventor (given name, family name)

**Thomas SPECHT**

Signature *Thomas Specht* Date 17.10.00

Residence Berlin, Germany DEX Citizenship Germany

Post Office Address Grabenstrasse 14, D-12209 Berlin, Germany

2-00 Full Name of additional joint inventor (given name, family name)

**Bernd HINZMANN**

Signature *Bernd Hinzmann* Date 17.10.00

Residence Berlin, Germany DEX Citizenship Germany

Post Office Address Parkstrasse 19, D-13127 Berlin, Germany

Full Name of additional joint inventor (given name, family name)

**Armin SCHMITT**

Signature \_\_\_\_\_ Date \_\_\_\_\_

Residence Berlin, Germany Citizenship Germany

Post Office Address Laubacher Strasse 6/II, D-14197 Berlin, Germany

Full Name of additional joint inventor (given name, family name)

4-00 **Christian PILARSKY**

Signature *Christian Pilarczyk* Date 17.10.00

Residence Schönfeld-Weissig, Germany DEX Citizenship Germany

Post Office Address Heinrich-Lange-Strasse 13c, D-01474 Schönfeld-Weissig, Germany

Full Name of additional joint inventor (given name, family name)

5-00 **Edgar DAHL**

Signature *Edgar Dahl* Date 17.10.2000

Residence Potsdam, Germany DEX Citizenship Germany

Post Office Address Eleonore-Procheska-Strasse 6, D-14480 Potsdam, Germany

■ Additional joint inventors are named on separately numbered sheets attached hereto.

Declaration for Patent Application (Continued)

**Correspondence Address:**  
MILLEN WHITE ZELANO & BRANIGAN, P.C.  
Suite 1400  
2200 Clarendon Boulevard  
Arlington, VA 22201  
TEL (703) 243-6333  
FAX (703) 243-6410

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

Full Name of sole or first inventor (given name, family name)

Thomas SPECHT

Signature	Date
Residence Berlin, Germany	Citizenship Germany
Post Office Address Grabenstrasse 14, D-12209 Berlin, Germany	

Full Name of additional joint inventor (given name, family name)

Bernd HINZMANN

Signature	Date
Residence Berlin, Germany	Citizenship Germany
Post Office Address Parkstrasse 19, D-13127 Berlin, Germany	

Full Name of additional joint inventor (given name, family name)

Armin SCHMITT

Signature <i>A. Schmitt</i>	Date October 18, 2000
Residence Berlin, Germany DEX	Citizenship Germany
Post Office Address Laubacher Strasse 6/II, D-14197 Berlin, Germany	

Full Name of additional joint inventor (given name, family name)

Christian PILARSKY

Signature	Date
Residence Schönfeld-Weissig, Germany	Citizenship Germany
Post Office Address Heinrich-Lange-Strasse 13c, D-01474 Schönfeld-Weissig, Germany	

Full Name of additional joint inventor (given name, family name)

Edgar DAHL

Signature	Date
Residence Potsdam, Germany	Citizenship Germany
Post Office Address Eleonore-Procheska-Strasse 6, D-14480 Potsdam, Germany	

■ Additional joint inventors are named on separately numbered sheets attached hereto.



## Declaration for Patent Application (Continued)

Full Name of additional joint inventor (given name, family name)

André ROSENTHAL

Signature

André Rosenthal

Date

17.10.2000

Residence

Berlin, Germany

DEX

Citizenship

Germany

Post Office Address

Koppenplatz 10, D-10115 Berlin, Germany

0022410044800